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OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 21:11:51 ; Search time 45 Seconds
                                            (without alignments)
                                   10392.935 Million cell updates/sec

Title: US-10-025-514-15
Perfect score: 1525
Sequence: 1 tctagaccatggaagaccct..........ccagtcaaggcctagtcgac 1525

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
            1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
            2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
            3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
            4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
            5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
            6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	629.4	41.3	1308	3	US-09-023-173-10	Sequence 10, Appl1
2	629.4	41.3	1308	3	US-09-023-339-6	Sequence 6, Appl1
3	628.4	41.2	1185	3	US-09-023-339-3	Sequence 3, Appl1
4	628.4	41.2	1260	3	US-09-023-173-5	Sequence 5, Appl1
5	429	28.1	1185	3	US-09-023-339-2	Sequence 2, Appl1
6	429	28.1	5932	4	US-09-299-141-4	Sequence 4, Appl1
7	429	28.1	6142	4	US-09-299-141-8	Sequence 8, Appl1
8	429	28.1	6565	4	US-09-299-141-1	Sequence 1, Appl1
9	429	28.1	6714	4	US-09-299-141-6	Sequence 6, Appl1
10	429	28.1	6924	4	US-09-299-141-9	Sequence 9, Appl1
11	429	28.1	6924	4	US-09-299-141-10	Sequence 10, Appl1
12	429	28.1	6924	4	US-09-299-141-11	Sequence 11, Appl1
13	429	28.1	6981	4	US-09-299-141-7	Sequence 7, Appl1
14	429	28.1	7054	4	US-09-299-141-3	Sequence 3, Appl1
15	429	28.1	7405	4	US-09-299-141-2	Sequence 2, Appl1
16	404.6	26.5	1356	3	US-08-481-534-16	Sequence 16, Appl1
17	404.6	26.5	1356	3	US-08-481-534-12	Sequence 12, Appl1
18	403	26.4	1356	1	US-08-002-202-12	Sequence 12, Appl1
19	403	26.4	1356	3	US-08-481-534-12	Sequence 12, Appl1
20	399.8	26.2	1356	3	US-08-002-202-18	Sequence 18, Appl1
21	399.8	26.2	1356	3	US-08-481-534-18	Sequence 18, Appl1
22	311.8	20.4	1339	1	US-07-859-480-1	Sequence 1, Appl1
23	227.2	14.9	7492	3	US-09-299-141-5	Sequence 5, Appl1
24	219.8	14.4	1423	1	US-07-829-954-1	Sequence 1, Appl1
25	219.8	14.4	1423	1	US-07-994-423-1	Sequence 1, Appl1
26	219.8	14.4	1423	1	US-08-421-891-1	Sequence 1, Appl1
27	207.8	13.6	10627	1	US-08-060-925A-12	Sequence 12, Appl
28	125.4	8.2	194	2	US-07-963-538B-5	Sequence 5, Appl1
29	124.6	8.2	2466	2	US-09-271-608-7	Sequence 7, Appl1
30	124.6	8.2	2466	4	US-09-695-950-7	Sequence 7, Appl1
31	124.6	8.2	2466	4	US-09-696-147-7	Sequence 7, Appl1
32	124.6	8.2	2466	4	US-09-696-364-7	Sequence 7, Appl1
33	123	8.1	180	3	US-08-483-503A-2	Sequence 2, Appl1
34	106.4	7.0	1508	3	US-08-660-347-1	Sequence 1, Appl1
35	81.6	5.4	1179	4	US-08-745-995A-22	Sequence 22, Appl1
36 c	81.6	5.4	1179	4	US-08-745-995A-23	Sequence 23, Appl1
37	81.6	5.4	1191	4	US-08-745-995A-4	Sequence 4, Appl1
38 c	81.6	5.4	1191	4	US-08-745-995A-5	Sequence 5, Appl1
39	81.6	5.4	1191	4	US-08-745-995A-34	Sequence 34, Appl1
40 c	81.6	5.4	1191	4	US-08-745-995A-35	Sequence 35, Appl1
41	81.6	5.4	1197	4	US-08-745-995A-10	Sequence 10, Appl1
42 c	81.6	5.4	1197	4	US-08-745-995A-11	Sequence 11, Appl1
43	81.6	5.4	1260	4	US-08-745-995A-16	Sequence 16, Appl1
44 c	81.6	5.4	1260	4	US-08-745-995A-17	Sequence 17, Appl1
45	81.6	5.4	1358	4	US-08-745-995A-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-023-173-10
; Sequence 10, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,168
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42995
; REFERENCE/DOCKET NUMBER: 0665-0007.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-023-173-10

Query Match   41.3%; Score 629.4; DB 3; Length 1308;
Best Local Similarity   70.8%; Pred. No. 8.9e-154;
Matches 837; Conservative   0; Mismatches 346; Indels   0; Gaps   0;

Qy   11 GGAAGACCCTCAAGGCGACGCGCCCTCAAAAAACCGACACCAGTCATCACGACGACCAAGACCA 70
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Mon Dec 9 12:50:40 2002

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Qy   1151 AAGCCCATTGTTTATGGGTAAGGTGTCAACCCAACTCAGAAG 1193
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Db   1256 GAGCCCCCTCTTCATGGGAAGGTCGTCAACCCACGCAGAAG 1298
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RESULT 2
US-09-023-339-6
; Sequence 6, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of `1-Antitrypsin
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,339
; FILING DATE: 13-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,991
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 0665-0003.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: codon-optimized No. 612714SI/XhoI fragment encoding RAmy3D
; CLONE: signal peptide-AAT fusion protein
US-09-023-339-6

Query Match   41.3%; Score 629.4; DB 3; Length 1308;
Best Local Similarity   70.8%; Pred. No. 8.9e-154;
Matches 837; Conservative   0; Mismatches 346; Indels   0; Gaps   0;

Qy   11 GGAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAAGACCA 70
Db   116 GGAGGACCCGCAGGGCGACGCCGCGCCCCAGAGACCGACACCAGCCACCAGCCAGGACCA 175

Qy   71 TCCGACTTTAATAAAATTACTCCAAGCTGAATTTGCTTTTCTTGTTTTTGTATAGACA 130
Db   176 CCCGACGTTCAACAAGATCACCCCGAATTTGGCCGAATTTGCCTTCAGCCTGTACCGCCA 235

Qy   131 ATTAGCTCATCAAAGTAATTCTACTAACATTTTTTAGTCCTGTTTCTATTGCCACTGC 190
Db   236 GCTCCGCACCAGTCCAACTCCACCAACATCTTCTTCAGCCCGGTGAGCATCGCCACCGC 295

Qy   191 TTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCCATGACGAGATTTTAGAAGGTTT 250
Db   296 CTTCGCCATGCTGTCCCTGGGTACCAAGGCGGACACCCCACGCGACGAGATCCTCGAAGGCT 355

Qy   251 AAACTTAATTTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTT 310
Db   356 GAACTTCAACCTGACGGAGATCCCGGAGGCCCAGATCCACGAGGGCTTCCAGGAGCTGCT 415

Qy   311 GAGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTCGTGTAACCGGTTTATTTTT 370
Db   416 CAGGACGCTCAACCAGCCGGACTCCCAGCTCCAGCTGACCACCCACGGGCTCTTCCT   475

Qy   371 GTCTGAAGGTTTAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAG 430
Db   476 GTCCGAGGGGCTCAAGCTCGTCGATAAGTTCCTGGAGGACGTGAAGAAGCTCTACCACTC 535

Qy   431 TGAGGCTTTACCGGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTA 490
Db   536 CGAGGCGGTTCACCGTCAACTTCGGGGACACCGAGGAGGCCAAGAAGCAGATCAACGACTA 595

Qy   491 TGTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATAC 550
Db   596 CGTCGAGAAGGGACCCAGGGCAAGATCGTGGACCTGGTCAAGGAATTGGACAGGGACAC 655

Qy   551 CGTCTTCGCACTAGTTAACATATATTTTTTCAAGGGTAAGTGGAACGTCCTTTCGAGGT 610
Db   656 CGTCTTCGCGCTCGTCAACTACATCTTCTTCAAGGGCAAGTGGGAGCGCCCGTTCGAGGT 715

Qy   611 TAAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAAT 670
Db   716 GAAGGACACCGAGGAGGAGGACTTCCACGTCGACCAGGTCACCACCGTCAAGGTCCCGAT 775

Qy   671 GATGAAAAGACTGGGTATGTTCAATATTGTTCAACATTGCAAAAAATTAAGTTCTTGGGTCTT 730
Db   776 GATGAAGAGGCTCGGCATGTTCAACATCGTTCAGCACTGCAAGAAGCTCTCCAGCTGGGTGCT 835

Qy   731 ATTAATGAAGTATTAGGTTAACGCTACTGCTATTTTTTTTTTTACCAGACGAAGGTAAGCT 790
Db   836 CCTCATGAAGTACCTGGGAACGCCACCGCCACCGCCATCTTCTTGCCGCCAGAGGGGCAAGCT 895

Qy   791 TCAACATTTGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGA 850
Db   896 CCAGCACCTGGAGAACGAGCTGACGCACGACATCATCCAGAAGTTCCTGGAGAACGAGGA 955

Qy   851 TCGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAA 910
Db   956 CAGGCGCTCGCTGCTAGCCTCACCTCCCACCTCCCCAAGCTACGGTACGTACGACCTGAA 1015

Qy   911 ATCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTCTACAGCGTCGTACGGTGCCGATTTGAGTGG 970
Db 1016 GAGCGTGCTGGGGCAGCTGGGCATCACGAAGGTCTTCAGCAACGGCGCGGACCTCTCCGG 1075

Qy   971 TGTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTAT 1030
Db 1076 CGTTGACGAGGAGGCCCCGCTGAAGCTCTCCAAGGCGGTCCACAAGGCGGTGCTCACGAT 1135

Qy 1031 TGATGAAAAGGGTACCGAGGCCCCGCTATGTTCCTGGAAGCATTCCAATGACGAT   1090
Db 1136 CGACGAGAAGGGACGGAGAAGCTCGCCGGGAGCTGCCATCCCCATGCTCCAT   1195

Qy 1091 TCCCACCAGAAGTTCAAGGTTAATAAAACCATTCGTTTTTGTTCCTTCGTGATGATGAGCAGAACACGAA 1150
Db 1196 CCCGCCCGAGGTCAAGTTCAACAAGCCCTTCGTCTTCCTGATGATCGAGCAGAACACGAA 1255
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;    NUMBER OF SEQUENCES: 22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Dehlinger & Associates
;      STREET: P.O. Box 60850
;      CITY: Palo Alto
;      STATE: CA
;      COUNTRY: USA
;      ZIP: 94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/023,339
;      FILING DATE: 13-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 60/037,991
;      FILING DATE: 13-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Petithory, Joanne R
;      REGISTRATION NUMBER: P42,995
;      REFERENCE/DOCKET NUMBER: 0665-0003.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 650-324-0880
;      TELEFAX: 650-324-0960
;    INFORMATION FOR SEQ ID NO: 3:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 1185 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      IMMEDIATE SOURCE:
;        CLONE: codon-optimized AAT coding sequence
US-09-023-339-3

Query Match             41.2%;  Score 628.4;  DB 3;  Length 1185;
Best Local Similarity   70.7%;  Pred. No. 1.6e-153;
Matches  836;  Conservative  0;  Mismatches  346;  Indels  0;  Gaps  0:
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Qy    12 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAAGACCAT  71
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Db     1 GAGGACCCCGCAGGCGACGCCGACGCCCAGAGAACCGACACCAGTCATCACGACCAAGACCAC  60

Qy    72 CCGACTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA 131
         |||||| || || ||||| |||||||||||||||||| ||| || |||||| || ||
Db    61 CCGACGTTCAACAAGATCACCCCGAATTTGGCCGAATTCGCCTTCCTGTACCGGCCAG 120

Qy   132 TTAGCTCATCAAAGTAATAATTCTACTAACATTTTTTTAGTCTGTTCTATTGCCACTGCT 191
         || ||| |||||||| | ||| | || ||||||||||||| ||||||||||||||||||||
Db   121 CTCCGCCACCAGTCCAACTCCAACAACATCTTCAGCCCCGGTGAGCATCGCCACCGCC 180

Qy   192 TTGCCATGTTGAGTTAGGTACTAAAGCCGATACCCATGACGAGATTTAGAAGGTTTA 251
         || |||||| | || |||||||||||| || ||||| ||||||||||| |||||||||
Db   181 TTCCCCATGCTGTCCCGGGTACCAAGGCGACCACCACGAGATCTCGAAGGGCTG 240

Qy   252 AACTTAATTGACCGAAATCCAGAAGAGCCCAAATTCAATTAACTACTGTAACGGTTGTTTG 311
         |||||||| ||||| ||||||||||| ||||||||||||| ||| ||||||||||||||||
Db   241 AACTTCAACCTGACGACGATCCCGAGGCGCAGATCCACCTCCAGCTCCACCACCGGCTGCTC 300

Qy   312 AGAACTTTGAATCAACCTGATTCAATTCCTAGAAGAACTATATCATAGT 371
         |||||| | || | ||||| ||||| ||||||||||| |||||||||||
Db   301 AGGACGCGTCAACACCGAGATCCCGGAGCTCCAGCTCACGACGACCTCCACCCTG 360

Qy   372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATACCTCC 431
         || ||||| || |||| || |||||||||||||||||||||||||||| ||||| |||
Db   361 TCCCAGGGCCTCAAGCTCGTCGATAAGTTCCTGGAGGACGTGAAGAGCCTCTACCACTCC 420

Qy   432 GAGGCTTTTACCGTTAATTTGGTGATACTGAGGAAGCAAATTAATGATTAT 491
         ||||| || ||||| || || | || || |||||||||||||||||||| ||
Db   421 GAGGCGTTCACCGTCACCTTCGGGGACACCGAGGAGGCCAAGAAGCAGATCAACGACTAC 480

Qy   492 GTTGAGAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
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Db   356 GAACTTCAACCTGACCGAGATCCCGGAGGCGCAGATCCACGAGGCTTCCAGGAGCTGCT 415
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Qy   311 GAGAACTTTGAATCAACCTGATTCAATTAACTACTGTAACGGTTTATTTTT 370

Db   416 CAGGACGCGTCAACCAGCCGACTCCCAGCTCCAGCTCCAGGCTCCAGGGCTCTTCCT 475
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Qy   371 GTCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAG 430

Db   476 GTCCCAGGGGCCTCAAGCTCGTCGATAAGTTCCTGGAGGACGTGAAGAGCCTCTACCACTC 535
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Qy   431 TGAGGCTTTTACCGTTAATTTGGTGATACTGAGGAAGCAAATTAATGATTA 490

Db   536 CGAGGCGTTCACCGTCAACTTCGGGGACACCGAGGAGGCCAAGAAGCAGATCAACGACTA 595
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Qy   491 TGTTGAGAAGGCACCCAGGGTAAGTCGTTAAAGAATTAGATCGTGATAC 550

Db   596 CGTCGAGAAGGGGGACCCAGGCAAGATCGTGACCTGGTCAAGGAATTGGACAGGGACAC 655
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Qy   551 CGTCTTCGCACTAGTTAACTATATTTTTTCAAGGTAAGTGGAACGTCCTTTCGAGGT 610

Db   656 CGTCTTCGCCGTCTGTCAACTACATCTTCTCAAGGGCAACTGGGAGCGCCCGTTCGAGGT 715
         ||||||||| ||| | |||||| || |||| ||||| ||| ||||| | ||| ||||||
Qy   611 TAAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAAT 670

Db   716 GAAGGACACCGAGGAGGAGGACTTCCACGTCGACCAGGTCACCACGGTCAAGGTCCCGAT 775
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Qy   671 GATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTT 730

Db   776 GATGAAGAGGCTCGGCATGTTCAACATCGCCACACTCCAGCACTGCAAGAGCCTCTCCAGCTGGGTGCT 835
         ||||| ||| || || |||||||||||  ||| | ||| ||||||||||| || ||| ||||||| |||
Qy   731 ATTAATGAAGTATTTAGGTAACGCTACTCGTATTTTTTTTTACCAGACGAAGTAAGCT 790

Db   836 CCTCATGAAGTACCTGGGGAACGCCACCCGCATCTTCTTCCTGCCGACGAGGCGCAAGCT 895
         | || |||||| | ||||| |||| ||| | || |||||||| ||||| |||  |||||
Qy   791 TCAACATTTAGAGAATGAGTTGACTCACTACCATCATGACAATTATTACTAAATTTTTAGAGAACGAGGA 850

Db   896 CCAGCACCTGGAGAACGAGCTGACGCACGACACCATCATGACGAGTTCCTGGAGAACGAGGA 955
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Qy   851 TCGTTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCCGTACTTACGACTTAA 910

Db   956 CAGGCGCTCCGCTAGCGTCCACCTCCCGAGCGTGAGCATCACCCGCACGTACGACCTGAA 1015
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Qy   911 ATCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTTCTAACGGTGCCGATTTGAGTGG 970

Db  1016 GAGCGTGCTGGGCCAGCTGGGCATCACGAAGGTCTTCAGCAACGCGGCGGACCTCTCCGG 1075
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Qy   971 TGTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTCACAAGAGCCGTCTTAACTAT 1030

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Qy  1031 TGATGAAAAGGGTACCGAGGCCGCGGCTATTGTCCTGGAAGCTATTCCAATGAGCAT 1090

Db  1136 CGACGAGAAGGGACGGAGCTCCGGGGAAGCTCCTGGAGGCCATCCCCATGTCCAT 1195
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Qy  1091 TCCACCAGAAGTAAAGTTAATTAATAAACCATTCGTTTTCTGTGATCGAGCAGAACACTAA 1150

Db  1196 CCCGCCGGAGGTCAAGTTCAACAAGCCCTTCGTCTTCCTGATGATCGAGCAGAACACGAA 1255
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Qy  1151 AAGCCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAAG 1193

Db  1256 GAGCCCGCCCCTCTTCATGGGGAAGGTCGTCAACCCCACGCAGAAG 1298
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RESULT 3
US-09-023-339-3
; Sequence 3, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of `1-Antitrypsin
; TITLE OF INVENTION: in Plants

```
;     CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/038,168
;     FILING DATE: 13-FEB-1997
;  ATTORNEY/AGENT INFORMATION:
;     NAME: Petithory, Joanne R
;     REGISTRATION NUMBER: P42995
;     REFERENCE/DOCKET NUMBER: 0665-0007.30
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-324-0880
;     TELEFAX: 650-324-0960
;  INFORMATION FOR SEQ ID NO: 5:
;  SEQUENCE CHARACTERISTICS:
;     LENGTH: 1260 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;  IMMEDIATE SOURCE:
;     CLONE: codon-optimized RAmy3D signal-mature AAT
US-09-023-173-5

Query Match             41.2%;  Score 628.4;  DB 3;  Length 1260;
Best Local Similarity   70.7%;  Pred. No. 1.6e-153;
Matches  836;  Conservative    0;  Mismatches  346;  Indels    0;  Gaps    0;

Qy     12 GAAGACCCTCAAGGCGACGGCCGTCAAAAAACCGACAACCAGTCATCACCAGGAAGACCAT 71
             | |||||| || ||||||||||||| |     ||||| ||||| ||| | || || | ||
Db     76 GGAGACCCCGCAGGGCGACGGCCGCCCAGAAGACCACCAGGACCACCACCAGGACCAC 135

Qy     72 CCGACTTTAATAAAATTACTCCAAATTTGCTTTTTCTTTGTATAGACAA 131
            ||||| ||  || || ||  |  |||||| || ||||| | ||  |   |
Db    136 CCGACGTTCAACAAGATCACCCCGAATTTGGCCGAATTCGCCTTCAGCCTGTACCGCCCAG 195

Qy    132 TTAGTCATCAAAGTAATTCTACTAACATTTTTTTAGTCCTGTTCTATTGCCACTGCT 191
            || | ||||| |  ||| ||| || |||| || | || |||  |  |||||||| |
Db    196 CTCGGCACCAGTCCAACTCCAACCAACATCTTCTTCAGCCCGGTGAGCATCGCCACCGCC 255

Qy    192 TTCGGCCATGTTGAGTTAGGTACTAAAGCCGATACCGATTTTAGAGAGGTTTA 251
            |||||||||| | || ||   ||| || || || ||||| |  | ||||  |||
Db    256 TTCGGCCATGCTGTCCCTGGGTACCAAGGCGACACCCAGAGATCCTCGAAGGGCTG 315

Qy    252 AACTTTAATTGACCCAAATCCCAGAAGCCCAAATTCACGAGGTTTTCAAGAGTTGTTG 311
            |||||  | | ||||  | ||| |||| |||||| || |||| || | |||||||| |
Db    316 AACTTCAACCTGACCGAGATCCCGAGCGCCGAGATCCCGAGCGGCGCTCCCAGGAGCTGCTC 375

Qy    312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGTTTATTTTTG 371
            || || | || || ||| |  || ||||  ||||| |||| ||||| |||||  |  |
Db    376 AGGACCGCCTCAACCAGCCAGCTCCCAGCTCCAGCTCCAGCCGCAACGGCGTCTTCCCTG 435

Qy    372 TCTGAAGGTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 431
            || || ||  ||| | ||| || |||||||| |||||| |||||||||| ||| || ||
Db    436 TCCGAGGGCCTTCAAGCTCGTCGATAAGTTCCTGGAGGACGTGAAGGAAGCTCTACCACTCC 495

Qy    432 GAGGCTTTTCACCGTTAATTTGGTGATACTGAGAGAAGCTAAAAAGCAAATTAATGATTAT 491
            ||||| || |||||| || | ||  ||| | || |  |||| ||| ||||  || || | |
Db    496 GAGGCGTTCACCGTCAACTTCGGGGACACCGAGGAGGCCAAGAGGCCAGATCAACGACTAC 555

Qy    492 GTTGAGAAAGGCACCCAGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
            || |||| ||| ||||||| ||||| || |||||  | ||||||||| ||  | ||||||
Db    556 GTCGGAGAGGGGACCCAGGGCAAGATCGTGGACCTGGTCAAGGAATTGGACAGGGACACC 615

Qy    552 GTCTTCGCACTAGTTAACTATATTTTTCTAAGGTAACGTCCTTTCGAGGTT 611
            ||||||||  | ||||||  | | |||||| ||| |||| ||| |||||||
Db    616 GTCTTCGCGGTCGTCAACTACATCTTCTTCAAGGGCAAGTTGGAGCGCCCCGTTCGAGGTG 675

Qy    612 AAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG 671
            ||| | ||||| |||| | ||| ||| |||| |||||| ||  | ||||| || |||||
Db    676 AAGGACACCGAGGAGGAGGACTTCCACGTCGACCAGGTCACCACCGTCAAGGTCCCGATG 735

Qy    672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTCACAATTAAGTTCTTGGGTCTTA 731
            |||||| | || || ||||||||||| || ||||| |  | ||| ||| |||| |||
Db    736 ATGAAGAGGCTCGGCATGTTCAACATCCAGCACTGCAGAAGCTCTCCAGCTGGGTGCTC 795
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Db    481 GTCGAGAAGGGGACCCAGGGCAAGATCGTGGACCTGGTCAAGGAATTGGACAGGGACACC 540
            || ||| |||| ||||||| ||||| || |||||  | ||||||||| ||  | ||||||
Qy    552 GTCTTCGCACTAGTTAACTATATTTTTCTAAGGTGGGAACGTCCTTTCGAGGTT 611
            ||||||||  | ||||||  | | |||||| ||| |||| ||| |||||||
Db    541 GTCTTCGCGGTCGTCAACATCTTCTTCAAGGGCAAGTGGGAGCGCCCCGTTCGAGGTG 600
            ||| | ||||| |||| | ||| ||| |||| |||||| ||  | ||||| || |||||
Qy    612 AAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG 671
            ||| | ||||| |||| | ||| ||| |||| |||||| ||  | ||||| || |||||
Db    601 AAGGACACCGAGGAGGAGGACTTCCACGTCGACCAGGTCACCACCGTCAAGGTCCCGATG 660
            |||||| | || || ||||||||||| || ||||| |  | ||| ||| |||| |||
Qy    672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTCAACAATTAAGTTCTTGGGTCTTA 731
            |||||| | || || ||||||||||| || ||||| |  | ||| ||| |||| |||
Db    661 ATGAAGAGGCTCGGCATGTTCAACATCCAGCACTGCAGAAGCTCTCCAGCTGGGTGCTC 720
            || |||| ||  ||| ||  | || ||  || |  ||||| ||  |  | | ||||  ||
Qy    732 TTAATGAAGTATTAGTTAACGCTACTGCTATTTTTTTTTACCAGACGAAGTAAGCTT 791
            || |||| ||  ||| ||  | || ||  || |  ||||| ||  |  | | ||||  ||
Db    721 CTCATGAAGTACCTGGGGAACGCCACCGCCATCTTCTTCCTGCCGGACGAGGGCAAGCTC 780
            || ||  || |||| || |||| || || || ||  | || | |  | |||| |||
Qy    792 CAACATTTAGAAATGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGAT 851
            || ||  || |||| || |||| || || || ||  | || | |  | |||| |||
Db    781 CAGCACCTGGAGAACGAGCTGGAACGCACGAGAGTTCCTGGAGAACCAGGAC 840
            ||  | || |  ||| || ||  ||  |  ||||| | | || || |||| ||  | ||
Qy    852 CGTCGTAGCGCGTTCTCTGCACCTGCCCAAAGTTAAGCTATCACCGGTACTTACGACCTGAAG 911
            ||  | || |  ||| || ||  ||  |  ||||| | | || || |||| ||  | ||
Db    841 AGGCGCTCCGGTAGCCTCCACCTCCCGAAGCTGACATCCGACGTACGACCTGAAG 900
            || || | ||||| || || || || || ||| |   || |  | |||| ||| | |||
Qy    912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTTCTAACGTGCCGATTTGAGTGGT 971
            || || | ||||| || || || || || ||| |   || |  | |||| ||| | |||
Db    901 AGCGTGCTGGGCCAGCTGGGCATCACGAAGGTCTTCAGCAACGGTCCGGACCTTCCGGC 960
            || || |||| || ||  | ||| || |||| ||  | | || || ||  | | ||||
Qy    972 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT 1031
            || || |||| || ||  | ||| || || |||| ||  | | || || ||  | | ||||
Db    961 GTGACGGAGGAGGCCCCCGTGAAGCTTCCAAGGCCGTGCTCACGACCG 1020
            || ||| || ||| || || || || || ||| || ||||| ||||  || ||| |||
Qy   1032 GATGAAAAGGGTACCGAGGCGCGGCGTATGTTCCTGGAAGCTATTCCAATGAGCATT 1091
            || ||| || ||| || || || || || ||| || ||||| ||||| ||||  || ||
Db   1021 GACGAGAAGGGGGACCGGAAGCTGCCGGGGCCATGTTCCTGGAGGCCATGTCCATC 1080
            || || || || || |||| ||  |  || |  ||||| ||||| ||||| || |||||
Qy   1092 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGACAGAAACACTAAA 1151
            || || || || |||| ||||| |  ||||||| |  || |||||||| ||||| || |||
Db   1081 CCGCCCGAGGTCAAGTTCAACAAGCCCTTCGTTCTTCGTCTGATGATCGAGCAGAACACGAAG 1140
            ||||| | || |||||||| ||| ||   |||| ||| || || ||||  ||||| |||
Qy   1152 AGCCCATTGTTTATGGGTAAGGTTGTCAACCAACTCAGAAG 1193
            ||||| | || ||||| | || | ||||| || | ||||||
Db   1141 AGCCCCCTCTTCATGGGAAGGTCGTCAACCCACGCAGAAG 1182
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RESULT 4
US-09-023-173-5
; Sequence 5, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
;   APPLICANT:  Sutliff, Thomas D.
;   APPLICANT:  Rodriguez, Raymond L.
;   TITLE OF INVENTION:  Production of Mature Proteins
;   TITLE OF INVENTION:  in Plants
;   NUMBER OF SEQUENCES:  23
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  Dehlinger & Associates
;    STREET:  350 Cambridge Ave., Suite 250
;    CITY:  Palo Alto
;    STATE:  CA
;    COUNTRY:  USA
;    ZIP:  94306
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Diskette
;    COMPUTER:  IBM Compatible
;    OPERATING SYSTEM:  DOS
;    SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/09/023,173
;    FILING DATE:  13-FEB-1998
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;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   CLONE: native AAT coding sequence
US-09-023-339-2

Query Match   28.1%;   Score 429; DB 3; Length 1185;
Best Local Similarity 60.2%;   Pred. No. 6.3e-102;
Matches 711;   Conservative   0; Mismatches 470; Indels 0; Gaps 0;

Qy   12 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAAGACCAT 71
Db   1 GAGGATCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCAC 60

Qy   72 CCGACTTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA 131
Db   61 CCAACCTTCAACAGATCACCCCCAACCTGGCTGAGTTGCGCCTTCAGCCTATACCGCCAG 120

Qy   132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTAGTCCTGTTTCTTATTGCCACTGCT 191
Db   121 CTGGCACCACCAGTCCAACAGCACCAATATCTTCTTCCCCCAGTGAGCATCGCTACAGCC 180

Qy   192 TTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGAGCAGAGATTTTAGAAGGTTTA 251
Db   181 TTTGCAATGCTCTCCCTGGGACCAAGGCTGACACTCACGAGGGTTTTCAAGAGTTGTTG 240

Qy   252 AACTTTAATTGACCGAAATCCCAGAAGCCAAATTCACGAGGCGTTTTGACCTGTATACC 311
Db   241 AATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCGCCATGAGAAGGCTTCCAGGAACTCCTC 300

Qy   312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTTATTTTG 371
Db   301 CGTACCCTCAACCAGCCAGACAGCAGCCAGCTCCAGCTGACCAGAGAGAACTATATCATAGT 360

Qy   372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAAACTATATCATAGT 431
Db   361 AGCGAGGGGCCTGAAGCTAGTGAAGTAGTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 420

Qy   432 GAGGCTTTTACCGTTAATTTGGTGATACTGAGGAAGCTAAAAGCAATTAATGATTAT 491
Db   421 GAAGCCTTCACTGTTAACTTCGGGGACCAGGACCTGCCCGTGGACGTGCCTATG 480

Qy   492 GTTGAGAAAGGCACCCAGGGTAAGATCCTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
Db   481 GTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGACACA 540

Qy   552 GTCTTCGCACTAGTTAACTATATATTTTTTCAAGGTAAGTGGGAAGTCCTTTCGGAGGTT 611
Db   541 GTTTTTGCTTCGTCGGTGAATTACATCTTTTTTTAAAGGCAAATGGGAGAGACCCCTTTGAGTC 600

Qy   612 AAAGATACTGAAGAGGAAGAGATTTCATGTGATCAAGTTGATCAAGTTACTACTGTCAAGTTCCAATG 671
Db   601 AAGGACACCGAGGAGAAGAGGACTTCCACGTGGACCACCGTGAAGGTGCCTATG 660

Qy   672 ATGAAAAAGACTGGGTATGTTCAATATTCAATATTCCAGCACTGTTAAGTATCACCGGTATCGTGATACC 731
Db   661 ATGAAGGGTTTTAGGCATGTTTAACATCCAGCACTGTTAAACATCCAGCACTGTTAAGTATCCTTCAGCCTGGGTGCTG 720

Qy   732 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTTACCAGACGAAGGTAAGCTT 791
Db   721 CTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGCCGGACGAGGGCAAACTA 780

Qy   792 CAACATTTAGAGAATGAGTTGACTCATGACATTATTACTAAATTTTAGAGAACGAGGAT 851
Db   781 CAGCACCTGGAAAATGAACTCATCACCAAGATATCATCACCAAGTTCCTGGAAAATGAAGAC 840

Qy   852 CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTAAGTTACGGTACTTACGACTTAAAA 911
Db   841 AGAAGGTCTGCGCGCTTACATTTTAACATTTTAACCCAAACTGTCCATTACTGGAAACTGTGATCGGAAG 900

Qy   912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTTCTACCGGTGCCGATTTGAGTGGT 971
Db   901 AGCGTCTGGGTCAACTGGGCATCACTAAGCGTCTTCAGCAATGGGGCATGGGGCTGCTCACTCTCCGGG 960

Qy   732 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTTACCAGACGAAGGTAAGCTT 791
Db   796 CTCATGAAGTACCTGGGGAACGCCACCGCCATCTTCTTCCTGCCGGACGAGGGCAAGCTC 855

Qy   792 CAACATTTAGAGAATGAGTTGACTCATGACATTATTACTAAATTTTAGAGAACGAGGAT 851
Db   856 CAGCACCTGGAGAACGAGCTGACGCACGACATCATCACCAAGTTCCTGGAAATGAGAGAC 915

Qy   852 CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTAAGTTACGGTACTTACGACTTAAAA 911
Db   916 AGGGGCTCCGCTAGCCTCCACCTCCGAGCTCCGAGCATCACCGGCACGTACGACCTGAAG 975

Qy   912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTTCTACCGGTGCCGATTTGAGTGGT 971
Db   976 AGCGTGCTGGGCAACTGGGCATCACTAAGCGTGCCGATCTGGGCAATGGGGCTGGTC 1035

Qy   972 GTTACTGAAGAAGTCCATTAAAATTGAGTAAAGCCGTCTCACAAAGCCGTCTTAACTATT 1031
Db 1036 GTGACGGAGGAGGCCCCCCTGAAGCTCTCCAAGGCCGTGCACAAGGCCGTGCTCACGATC 1095

Qy 1032 GATGAAAAGGGTACCGAGGCGCCGGCCTATGTTCCTGGAAGCTATTCCAATGAGCATT 1091
Db 1096 GACGAGAAGGGGACGGAAGCTGCCGGGCCATGTTCCTGGAGGCCATCCCCATGTCCATC 1155

Qy 1092 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA 1151
Db 1156 CCGCCCGAGGTCAAGTTCAACAAGCCCTTCGTCTTCGTGATGATCGAGCAGAACACGAAG 1215

Qy 1152 AGCCCATTGTTTATTGGGTAAGGTTGTCAACCAACTCAGAAG 1193
Db 1216 AGCCCCCTCTTCATTGGGGAGGTCGTCAACCCCCACGCGCAAG 1257

RESULT 5
US-09-023-339-2
; Sequence 2, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
; ,,   APPLICANT: Sutliff, Thomas D.
; ,,   APPLICANT: Rodriguez, Raymond L.
; ,,   TITLE OF INVENTION: Production of '1-Antitrypsin
; ,,   TITLE OF INVENTION: in Plants
; ,,   NUMBER OF SEQUENCES: 22
; ,,   CORRESPONDENCE ADDRESS:
; ,,   ADDRESSEE: Dehlinger & Associates
; ,,   STREET: P.O. Box 60850
; ,,   CITY: Palo Alto
; ,,   STATE: CA
; ,,   COUNTRY: USA
; ,,   ZIP: 94306
; ,,   COMPUTER READABLE FORM:
; ,,   MEDIUM TYPE: Diskette
; ,,   COMPUTER: IBM Compatible
; ,,   OPERATING SYSTEM: DOS
; ,,   SOFTWARE: FastSEQ for Windows Version 2.0
; ,,   CURRENT APPLICATION DATA:
; ,,   APPLICATION NUMBER: US/09/023,339
; ,,   FILING DATE: 13-FEB-1998
; ,,   PRIOR APPLICATION DATA:
; ,,   APPLICATION NUMBER: 60/037,991
; ,,   FILING DATE: 13-FEB-1997
; ,,   ATTORNEY/AGENT INFORMATION:
; ,,   NAME: Petithory, Joanne R
; ,,   REGISTRATION NUMBER: P42.995
; ,,   REFERENCE/DOCKET NUMBER: 0665-0003.30
; ,,   TELECOMMUNICATION INFORMATION:
; ,,   TELEPHONE: 650-324-0880
; ,,   TELEFAX: 650-324-0960
; ,, INFORMATION FOR SEQ ID NO: 2:
; ,,   SEQUENCE CHARACTERISTICS:
; ,,   LENGTH: 1185 base pairs
; ,,   TYPE: nucleic acid
; ,,   STRANDEDNESS: single

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Qy   972 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT 1031
         |||| || || || ||  || || ||  || || ||  ||||
Db   961 GTCACAGAGGAGGCACCCCTGAAGCTCTCCAAGCCGTGCATAAGGCTGTGCTGACCATC 1020

Qy  1032 GATGAAAAGGGTACCGAGGCCGCCGGCCGTATGTTCCTGGAAGCTATTCCAATGAGCATT 1091
         || || || || ||||  || ||  || ||||
Db  1021 GACGAGAAAGGGACTGAAGCGTGCTGGGCCATGTTTTTAGAGGCCATACCCGTGTCTATC 1080

Qy  1092 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGCAGAACTAAA 1151
         || ||  || ||||  || ||  ||
Db  1081 CCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAG 1140

Qy  1152 AGCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAA 1192
         | ||| ||||| ||
Db  1141 TCTCCCCTCTTCATGGGGAAAAGTGTGAATCCCACCCAAAA 1181
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Query Match         28.1%;  Score 429;  DB 4;  Length 5932;
Best Local Similarity   60.2%;  Pred. No. 1.1e-101;
Matches  711;  Conservative   0;  Mismatches 470;  Indels   0;  Gaps   0;

Qy    12 GAAGACCCTCAGGCGACGCCGCTCAAAAAACCGACAACCAGTCATCACGACCACAGACCAT 71
         || || || || ||||  || ||  |||| || || ||||  ||||  ||
Db  1385 GAGGATCCCCGAGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCAC 1444

Qy    72 CCGACTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA 131
         || ||  ||||| || ||  |||| ||  |||
Db  1445 CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTATACCGCCCAG 1504

Qy   132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTAGTCCTGTTTCTATTGCCACTGCT 191
         | ||  ||||  || || ||  |||
Db  1505 CTGGCACCACCAGTCCAACAGCACCAATATCTTCTTCCCCCAGTGAGCATCGCTACAGCC 1564

Qy   192 TTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCGATACGAGATTTAGAAGTTTA 251
         |  || || ||  | || ||||
Db  1565 TTTGCAATGCTCTCCCTGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTG 1624

Qy   252 AACTTAATTTGACCGAAATCCCAGAGCCCAAATTCAGCAGGGTTTTCAAGAGTTGTTG 311
         || |||||  || ||||  ||  || ||||
Db  1625 AATTTCAACCTCACGGAGATTCCGGAGGCTTCCAGGAAGCTTCCAGGAACTCCTC 1684

Qy   312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG 371
         | |||||  || || |||  || ||  ||||
Db  1685 CGTACCCCTCAACCAGCCCAGAGCAGCCAGCTCCAGCTGACCACCGGCAATGGCCGTGTTCCTC 1744

Qy   372 TCTGAAGGTTTAAAATTGGTTGACAAATTGTGACAAATTCCTAGAAGACGTCAAGAAACTATCATCATAGT 431
         |  || |||||  || ||  || ||||
Db  1745 AGCGAGGGGCCTGAAGCTAGTAGTCAGCTAGTAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 1804

Qy   432 GAGGCTTTACCGTTAATTGTGTGATACTGAGGAGCTAAAAGCAAATAATGATTAT 491
         || || || || ||||  || ||  |||| ||||
Db  1805 GAAGCCTTCACTGTCAACTTCGGGGACACCGAGAGGCCGAGAGACAGATCAACGATTAC 1864

Qy   492 GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
         |  |||| || ||||  || || ||  || |||
Db  1865 GTGGAGAAGGGTACTCAAGGGAAAATGTGGATTGGTCAAGAGCTTGACAGAGACACA 1924

Qy   552 GTCTTCGCACTAGTTAACTATATTTTTCAAGGTAGTGAGGTAGTGGGAACGTTCCTTTCGAGGTT 611
         || || || ||||  || ||||  || ||
Db  1925 GTTTTTGCTTGGTGAATTACATCTTCTTAAAGGCAAATGGGAGAGACCCTTTGAAGTC 1984

Qy   612 AAAGATACTGAAGAGGAAGAGATTTTCATGTGATCAAGTTACTACTGTCAAAGTTCCAATG 671
         || |||||| ||||  || || |||
Db  1985 AAGGACACCGAGGAAGAGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATG 2044

Qy   672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTGGGTCTTA 731
         |||||  | ||||  ||||| || || || || ||
Db  2045 ATGAAGCGGTTTAGGCATGTTAACATCCAGCACTGTAAGAAGCTGTCCAGCTGGGTGCTG 2104

Qy   732 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTTTTACCAGACGACGAAGGTAAGCTT 791
         | |||||  || || || ||||  || ||  ||
Db  2105 CTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAACTA 2164

Qy   792 CAACATTTAGAGATGAGTTGACTCATGACATTATTACTAAATTTTAGAAGAACGAGGAT 851
         || || |||  | ||||  ||||  ||
Db  2165 CAGCACCTGGAAAATGAACTCACCCACGATATCATCACCAAGTTCCTGGAAAAATGAAGAC 2224

Qy   852 CGTCGTAGCGCTTCTCTGCCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA 911
         || || || |||  ||  |||| || ||  |||
Db  2225 AGAAGGTCTGCCAGCTTACATTTACCAAACTGTCCATTACTGGAACCTATGATCGAAG 2284

Qy   912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTCTAACGTGCCGATTTGAGTGT 971
         || || ||  || || ||  |||| || ||  |||
Db  2285 AGCGTCCTCGGGTCAACTGGGCATCACTAAAATTGAGTAAAGCCGTGTGTCACAAACCG 2344

Qy   972 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAACCGTCTTAACTATT 1031
         |  || || || ||  || || ||  ||||
Db  2345 GTCACAGAGGAGGCACCCCCTGAAGCTCTCCAAGCCCATAAGGCTGTGCTGACCATC 2404

Qy  1032 GATGAAAAGGGTACCGAGGCCGCCGGCCGTATGTTCCTGGAAGCTATTCCAATGAGCATT 1091
         || || || || ||||  || ||  || ||||
Db  2405 GACGAGAAAGGGACTGAAGCGTGTGGGCCATGTTTTTAGAGGCCATACCCATGTCTATC 2464

Qy  1092 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGCAGAACTAAA 1151
         || ||  || ||||  || ||  ||
Db  2465 CCCCCGAGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAG 2524

Qy  1152 AGCCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAA 1192
         | ||| ||||| ||
Db  2525 TCTCCCCTCTTCATGGGAAAAGTGGTGAATCCACCCACCCAAAA 2565
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;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43mSENC-AT
US-09-299-141-8

Query Match             28.1%;  Score 429;  DB 4;  Length 6142;
Best Local Similarity   60.2%;  Pred. No. 1.1e-101;
Matches  711;  Conservative    0;  Mismatches  470;  Indels    0;  Gaps    0;

Qy         12 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACCACCAGTCATCACGACCAAGACCAT 71
              || ||| ||  || ||| || || ||  ||   || | |    || || ||   || | ||
Db       1595 GAGGATCCCCAGGGAGGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCAC 1654

Qy         72 CCGACTTTTAATAAATTACTCCGAATTTGCTTTTTCTTTGTATAGACAA 131
              || | ||| ||| ||  |  | ||| |  || ||  | | |   |  || |
Db       1655 CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTATACCGCCAG 1714

Qy        132 TTAGCTCATCAAAGTAATTCTACTAACACATTTTTTAGTCCTGTTCTATTGCCACTGCT 191
              ||  | || |  |  ||  || || | ||| |   | |||  |  |  | || ||| |||
Db       1715 CTGGCACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGACGATCGCTACAGCC 1774

Qy        192 TTCGCCATGTTGAGTTTGGTTAGGTACTAAAGCCGATACCCATGACGAGGATTTTAGGTTTA 251
              || || ||||||   | || || |  | ||| || |  ||| ||||  | ||||   || ||
Db       1775 TTTGCAATGCTCTCTCCCTGGGGACCAAGGCTCACGATGAAATCCACGATCAGGATCAC 1834

Qy        252 AACTTTAATTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTG 311
              | || |||   |  ||| ||| || || |  ||||||| || | || || || | |
Db       1835 AATTTCAACCTCACGGAATTCCGGAGGCTCAGATCCATGAAGCCTTCCAGGAACTCCTC 1894

Qy        312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG 371
              | || |||  ||| || | ||| || ||||  | ||| || | || ||| |||  | |
Db       1895 CGTACCCTCAACCAGCCAGAGCTCCAGCTGACGATGGCCTGTTCCTC 1954

Qy        372 TCTGAAGGTTAAAAATTGGTTGACAAATCCTAGAGAGACGTCAAGAAAAACTATATCATAGT 431
              | || || ||| |   |||| || ||| ||  ||  | || ||| ||  |  | | |||
Db       1955 AGCGAGGGCCTGAAGCTAGTGATAGTTTGGATGATGTTAAAAGTTGTACCACTCA 2014

Qy        432 GAGGCTTTTACCGTTAATTTGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT 491
              | || ||| || |||  |  | | | |  ||| ||||   ||| || ||  | | |
Db       2015 GAAGCCCTTCACTGTCAACTTCGGGGACCAGCCAAGAGAGCCAAGAAACAACGATTAC 2074

Qy        492 GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
              || || |||| || || || ||| || ||| | | ||| ||||||| ||| ||| ||||
Db       2075 GTGGAGAAGGGTACTCAAGGGAAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACA 2134

Qy        552 GTCTTCGCACTAGTTAACTATATATTTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTT 611
              || || || || ||  ||| | | |  | |  ||| |  ||| || |  |  | | |||||
Db       2135 GTTTTGCTCTGGTGAATTACATCTTCTTTTAAAGGCAAATGGGAGGACCCCTTGAAGTC 2194

Qy        612 AAAGATACTGAAGAGAGAGATTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG 671
              | | ||| || | || | |||| ||| || | |||| | | |  | ||||  ||| ||
Db       2195 AAGGACACCGAGGAGGAGGACTTCCCACGTGGACCACCGTGACCACCGTGAAGGTGCCTATG 2254

Qy        672 ATGAAAAGACTGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA 731
              || ||| ||| ||||||||||   |  |||| | |||    |||| |||| ||| | |
Db       2255 ATGAAGACTGTTTAGGCATGTTTAACATCCAGCTGCCAGCGTGGGTGCTG 2314

Qy        732 TTAATGAAGTATTTAGGTAACCCTGCTATTTTTTTTTACCGTGAAGGAAGGTAAGCTT 791
              || ||| ||| |  ||| ||||  || ||| | |  |  | ||| | | |||| | ||
Db       2315 CTGATGAAATACCTGGCAATGCCGTCATCTTCCTGCCTGATGAGGGGAAACTA 2374

Qy        792 CAACATTTAGAAGATGAGTGACTCATGAAATCATTACTAACTAAATTTTTAGAGAACGAGGAT 851
              |  || |||| | |||| || | || |   | |  | |  | ||| || | ||||  ||| |
Db       2375 CAGCACCCTGGAAAATGAACTTCACCACCAGTTCCTGGAAAATGAAGAC 2434

Qy        852 CGTCGTAGCCGCTTCTCTGCACCTGCCAAAGTAAGTAAGTATCACCGGTACTTACGACTTAAAA 911
              || | |  || |||  | ||  |||  || || || || | |  || | | ||  ||| ||||
Db       2435 CAGCACCTGGAAAATGAACTGACTTTACATTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAG 2494

Qy        912 TCTGTTTTAGGCCAGTTAGGTATTACCCAAAGTTTTTCTAACGGTGCCGATTTGAGTGGT 971
              | ||||  ||| ||| ||| || | ||| ||||| | ||| ||| || | | | ||  |
Db            CGTACCCTCAACCAGCCAGCAGCTCCAGCTGACCACCGTGAAGGTGCCTGTTCCTC 1303
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Db       2495 AGGCTCCTGGGTCAACTGGGCATCACTGGGCATTAAAATTGGCATCACTAAGGGTGACCTGACCTCTCCGGG 2554
              || ||    || || ||  ||||   ||  | || ||||||  || |  || |  ||  | || ||||| |
Qy        972 GTTACTGAAGAGCTCCATTAAATTGGAGTAAGCTGTTCACAAAGCCGTCTTAACTATT 1031
Db       2555 GTCACAGAGGAGGCACCCTCGAGCTCTCCAAGGCCGTGCGTGCATAAGGCGTGTGCTGACCATC 2614
              || |  || | | |||  | || ||| || || |  |    ||   || |||| |  ||
Qy       1032 GATGAAAAGGGTACCAGGCCCGGCCGTATGTTCCTGGAAGCTATTCCAATGAGCATT 1091
Db       2615 GACGAGAAAGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATC 2674
              || |  ||||| || || || || || |||||||   | ||| ||  | | ||| |||
Qy       1092 CCACCAGAAGTAAATTTAAATAAAACATTCGTTTTCTGATGATCGAGCAGAAACACTAAA 1151
Db       2675 CCCCCGAGGTCAAGTTCAACAAACCCTTTGCTCTTCTTAATGATTGAACAAAATACCAAG 2734
              ||  | || || |  ||||  | |  || ||  | | | | |||| || || | || |||
Qy       1152 AGCCCATTGTTATGGGTAAGGTGTCAACCCAACTCAGAA 1192
Db       2735 TCTCCCCTCTTCATGGGAAAGTGGTGAATCCCACCCAAAA 2775
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```
RESULT 8
US-09-299-141-1
; Sequence 1, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6565
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID C-AT
US-09-299-141-1

Query Match             28.1%;  Score 429;  DB 4;  Length 6565;
Best Local Similarity   60.2%;  Pred. No. 1.1e-101;
Matches  711;  Conservative    0;  Mismatches  470;  Indels    0;  Gaps    0;

Qy         12 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACCACCAGTCATCACGACCAAGACCAT 71
              || ||| ||  || ||| || || ||  ||   || | |    || || ||   || | ||
Db        944 GAGGATCCCCAGGGAGGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCAC 1003

Qy         72 CCGACTTTTAATAAATTACTCCGAATTTGCTTTTTCTTTGTATAGACAA 131
              || | ||| ||| ||  |  | ||| |  || ||  | | |   |  || |
Db       1004 CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTATACCGCCAG 1063

Qy        132 TTAGCTCATCAAAGTAATTCTACTAACACATTTTTTAGTCCTGTTCTATTGCCACTGCT 191
              ||  | || |  |  ||  || || | ||| |   | |||  |  |  | || ||| |||
Db       1064 CTGGCACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGACGATCGCTACAGCC 1123

Qy        192 TTCGCCATGTTGAGTTTGGTTAGGTACTAAAGCCGATACCCATGACGAGGATTTTAGGTTTA 251
              || || ||||||   | || || |  | ||| || |  ||| ||||  | ||||   || ||
Db       1124 TTTGCAATGCTCTCCCTGGGGGACCAAGGCTGACACTCACGATGAAATCCACGATCAGGAAACTA 1183

Qy        252 AACTTTAATTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTG 311
              | || |||   |  ||| ||| || || |  ||||||| || | || || || | |
Db       1184 AATTTCAACCTCACGGAATTCCGGAGGCTCAGATCCATGAAGCCTTCCAGGAACTCCTC 1243

Qy        312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG 371
              | || |||  ||| || | ||| || ||||  | ||| || | || ||| |||  | |
Db       1244 CGTACCCTCAACCAGCCAGCAGCTCCAGCTGACGATGATCGACAACTGGAACCTATGATCTGAAG 1303

Qy        372 TCTGAAGGTTAAAAATTGGTTGACAAATCCTAGAGAAGACGTCAAGAAAACTATATCATAGT 431
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; SEQ ID NO 6
; LENGTH: 6714
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID
; OTHER INFORMATION: p43CB-AT
US-09-299-141-6

Query Match    28.1%;   Score 429;  DB 4;  Length 6714;
Best Local Similarity   60.2%;   Pred. No. 1.1e-101;
Matches  711;  Conservative  0;  Mismatches  470;  Indels  0;  Gaps  0;

Qy      12 GAAGACCCTCAAGGCGACGCCGTCAAAAAACCGACACCAGTCATCACGACCAAGACCAT   71
            ||||| || || ||  | || | |||||| ||||  || ||||||  ||| | |||||
Db    2167 GAGGATCCCCAGGGAGATGCTGCCCAGAGACAGATACATCCCACCATGATCAGGATCAC 2226

Qy      72 CCGACTTTTAATAAAATTACTACCAAATTTGCTTTTCTTCTTGTATAGACAA   131
            || ||| |  ||  | || || ||| || || |||||| ||   |  | |||
Db    2227 CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTATACCGCCAG 2286

Qy     132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTAGTCCTGTTTCATTGCCCACTGCT   191
            |  || | ||   || |  | | | | |    |  | ||  ||||  |||| || |||
Db    2287 CTGGCACACCAGTCCAACAGCACCAATATCTTCTCTCCCCAGTGACGCATCGCTACAGCC 2346

Qy     192 TTCGGCCATGTGAGTTAGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA   251
            | | | |  |||  ||  ||  | | |||| || |   | || |   ||  |  ||||
Db    2347 TTTGCAATGCTCTCCCTGGGACCAAGGCTGCACACTCACGATGAAATCCTGGAGGGCCTG 2406

Qy     252 AACTTTAAATTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTG   311
            | |  | |   ||||||| ||| || || ||  | ||| | |  ||| || |||  |
Db    2407 AATTTCAACCTCACGGAGATTCGGGACGTTCAGATCGAAGCTTCAGGACTCCTC 2466

Qy     312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTGTTTATTTTG   371
            || || | || || || || |  | |||| ||||||||  | ||  |||| ||  ||||
Db    2467 CGTACCCTCAACCAGCAGACAGCCAGTTCCAGCGCCAATGGCCAATGGCCTGTTCCTC 2526

Qy     372 TCTGAAGGTTAAAATTGGTTGACATCCTGATACGTGAGAAGACTCAAGAAACTATATCATAGT   431
            | || || | |||  | |  || |   ||   || | || || || || |  | | | |
Db    2527 AGCGGTCCTGGTCAACTGCACTACTGCTTACCTCAGCCTACTAAGGCTCGAATGGGGCTGACCTCTCCGGG 2586

Qy     432 GAGGCTTTACCGTTAATTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT   491
            |||| || ||  | |   | || ||| || || || || |  ||||  || ||||||
Db    2587 GAAGCTTCACTGTCAACTTCGGGGACCTAGTTGCTGCCATTCCAATGAGCATT 2646

Qy     492 GTTGAGAAAGGCACCCAGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC   551
            |||||||| ||||||||| |  || || |  ||||| || |||| ||||  |||||||
Db    2647 GTGGAGAGGTACTCACGGGAAAATTGTGCAAGGAGCTTGGTCAAGAGACACA 2706

Qy     552 GTCTTCGCACTAGTTAACTATATATTTTTCAAGGTAAGTGGGAACGTCCTTTCGAGGTT   611
            || ||  |  | || |||| | | || |||| |  || || || || ||||| |||||
Db    2707 GTCTTCGCCACTAGTTAACTATATTTTTCATGTGATCAAGTTACTACTGTCCCGTGAAGTC 2766

Qy     612 AAAGATACTGAAGAGGAGAGATTTCATGTTGATCAAGTTACTGCTGTCAAGTTCCAATG   671
            ||||| || || |||| ||| || |||| || |||||||||| ||||||||| |||||
Db    2767 AAGGACACCGAGGAAGAGAGGACTTCCACGTGACCAGGTGCCATG 2826

Qy     672 ATGAAAAGACTGGGTATGTTCAATATTCAATATTGCAAAAAATTAAGTTCTTCGGTCTTA   731
            |||||| || || | | | |  | |   || || ||  |   ||  |  | | || |||
Db    2827 ATGAGAGCGTTTAGGCATGTTTAACATCCAGCACACTGTAAGAAGCTGTCCAGCTGGTGCTG 2886

Qy     732 TTAATGAAGTATTAGGTAACGCTACTGCTATTTTTTTTACCAGACGAGGGTAAGCTT   791
            || | ||| || ||  | || || ||  | |   |  | || |  ||| || |||||
Db    2887 CTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTCTCCTGCTAGATGCTCTATC 2946

Qy     792 CAACATTTAGAAGATGAAGTTGACTCATGACCTAAATTTTTAGAGAACGAGGAT   851
            ||||| |||||| || || || || ||  |||||  |  | || || ||||||
Db    2947 CAGCACCTGAAAATGAACGATCACCACGATAATCACCAAGTTCCTGGAGAAATGAAGAC 3006

Qy     852 CGTCGTAGCGCTTCTCCACCTGCCAAAGTTAGTATCACCGTACTTAAA   911
            || |||||||||| | || |  || | | |  ||| || |  ||||||
Db    3007 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTTCCATTACTGGAACCTATGATCTGAAG 3066


Db    1304 AGCGAGGGGCCTGAAGCTAGTGGATAAGTTTGGAGGATGTTAAAAAGTTGTACCACTCA 1363
            || ||| || ||||||| ||| |  | ||| |||||  | || |||||| ||||||||
Qy     432 GAGGCTTTACCGTTAATTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT 491

Db    1364 GAAGCCTTCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAACAGATCAACGATTAC 1423
            || || || |||||||||||  |  || |||| || || |||| ||| || ||||||
Qy     492 GTTGAGAAAGGCACCCAGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551

Db    1424 GTGGAGAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACA 1483
            || ||| ||||||| |||| ||||||||  || | ||||| || ||||| ||| ||||
Qy     552 GTCTTCGCACTAGTTAACTATATATTTTTCAAGGTAAGTGGGAACGTCCTTTCGAGGTT 611

Db    1484 GTTTTTGCTCTGGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGAAGTC 1543
            || ||| | |  |||||| ||| | ||  |||| | |||||||   |  || |||||||
Qy     612 AAAGATACTGAAGAGGAGAGATTTCATGTTGATCAAGTTACTGCTGTCAAGTTCCAATG 671

Db    1544 AAGGACACCGAACAGGAAGAGAGGACTTCCACGTGACCAGGTGCCACCGTGAAGGTGCCTATG 1603
            |||||  || ||  || |||| || || |||| || |||| || || |  ||||| ||||||
Qy     672 ATGAAAAGACTGGGTATGTTCAATATTCAATATTGCAAAAAATTAAGTTCTTCGGTCTTA 731

Db    1604 ATGAGAGCGTTTAGGCATGTTTAACATCCAGCACACTGTAAGAAGCTGTCCAGCTGGTGCTG 1663
            || || | | | |   | | || |  | |||| || || | || ||  ||| || | |
Qy     732 TTAATGAAGTATTAGGTAACGCTACTGCTATTTTTTTTACCAGACGAGGGTAAGCTT 791

Db    1664 CTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTCTCCTGCTAGATGCTCTATC 1723
            ||  ||||||||||  | || ||  |  | || | |  | || || || ||  |||
Qy     792 CAACATTTAGAAGATGAAGTTGACTCATGACCTAAATTTTTAGAGAACGAGGAT 851

Db    1724 CAGCACCTGAAAATGAACGATCACCACGATAATCACCAAGTTCCTGGAGAAATGAAGAC 1783
            ||  || ||||| ||||  || ||  ||  | ||  | | || ||||| |  ||||||
Qy     852 CGTCGTAGCGCTTCTCCACCTGCCAAAGTTAGTATCACCGTACTTAAA 911

Db    1784 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTTCCATTACTGGAACCTATGATCTGAAG 1843
            || || |||||| |  |  |  ||| || |||| || || ||  || | ||  || ||||
Qy     912 TCTGTTTTAGGCCAGTAGTATTACCAAAGTTTTTCTACACGTGCCGATTTGAGTGGT 971

Db    1844 AGCGTCCTGGTCAACTGCACTACTGCTTACCTCAGCCTACTAAGGCTCGAATGGGGC 1903
            || ||  || |||| | || ||||   || |  | | | ||  | || |  |||||
Qy     972 GTTACTGAAGAAGCTCCATTAAAATTGAGTGAAAGCCGTGTTCACAAAGCCGTGTTCACTATT 1031

Db    1904 GTCACAGAGGAGCCACCCCGGGCGCCGCCGGCTATGTTCCTCAAGGCCATCGATAAGGCGT 1963
            || | || || ||  |  ||| || || || | || || || || ||  |||  | ||
Qy    1032 GATGAAAAGGCACCCGAGGCGCCGGCCCGGTATGTTCCTGGAAGCTATTCCAATGAGCATT 1091

Db    1964 GACGAGAAAGGGACTGAAGCTGTCTGCGGGCCATGTTTAGGCCATGGCCATCGTGATACCATC 2023
            || || ||||| || ||||| ||  | || || | |  || || ||  | | || |||  |
Qy    1092 CCACCAGAGTAAATTTAATAACACCAACCCTTTGTCTTTTTGTGATGATCGAGGAACACTAA 1151

Db    2024 CCCCCGAGGTCAAGTCAACAAACCCTTTGTGTCTTCTTTAATGATTGAACAAAATACCAAG 2083
            ||||| || |||| |||||  ||| || ||| | |  ||  || || ||| ||||||||
Qy    1152 AGCCCATTGTTATGGGTAAGGTTGTCAACCCAACTCAGAA 1192

Db    2084 TCTCCCCTCTTCATGGAAAAGTGTGAATCCCACCCAAA 2124
```

RESULT 9
US-09-299-141-6
; Sequence 6, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0

Qy   912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTCTAACGTGCCGATTTGAGTGGT 971
           || |||||| || || || | ||| ||||| || || ||
Db   3067 AGGGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGCTGACCTCTCCGGG 3126

Qy   972 GTTACTGAGAGAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT 1031
           || || || ||| ||| || || | || || ||||||||||| |||| || ||
Db   3127 GTCACAGAGGAGGACCCCTGAGCTCTCAAGGCCGTGCATAAGGCTGTGCTGACCATC 3186

Qy   1032 GATGAAAAGGGTACCGAGGCGCCGCCTATGTTCCTGGAAGCTATTCCAATGAGCATT 1091
           || ||||||| || || || || || |||| || ||| || |||| || ||||
Db   3187 GACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATC 3246

Qy   1092 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGCAGAACACTAA 1151
           ||||||||||| || |||| | || ||| || || ||||| || || ||
Db   3247 CCCCCGAGGTCAAGTTCAACAAACCCTTGTCTTCTTAATGATTGAACAAAATACCAAG 3306

Qy   1152 AGCCCATTGTTTATGGGTAAGGTTGTCAACCAACTCAGAA 1192
           || ||| ||| ||||||||||| || |||| | ||
Db   3307 TCTCCCCTCTTCATGGGAAAAGTGGTGAATCCACCCAAAA 3347

RESULT 10
US-09-299-141-9
; Sequence 9, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;   APPLICANT: FLOTTE, TERENCE R.
;   APPLICANT: SONG, SIHONG
;   APPLICANT: BYRNE, BARRY J.
;   APPLICANT: MORGAN, MICHAEL
;   TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;   FILE REFERENCE: 4300.011800
;   CURRENT APPLICATION NUMBER: US/09/299,141
;   CURRENT FILING DATE: 1999-04-23
;   EARLIER APPLICATION NUMBER: 60/083,025
;   EARLIER FILING DATE: 1998-04-24
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 9
;   LENGTH: 6924
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43rmsENC-AT
US-09-299-141-9

  Query Match   28.1%; Score 429; DB 4; Length 6924;
  Best Local Similarity 60.2%; Pred. No. 1.1e-101;
  Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

Qy   12 GAAGACCCTCAAGGCGACGCGCCTCAAAAACCGACACCAGTCATCACGACCAAGACCAT 71
           || ||| |||| || || || || || || ||||| ||| || || | || |
Db   2377 GAGGATCCCCAGGGAGATGCTCCCCAGGACGAGATCACATCCACCATGATCAGGATCAC 2436

Qy   72 CCGACTTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTTTCTTTGTATAGACAA 131
           || |||| ||| | || ||| | ||| ||| ||||| || || || || ||
Db   2437 CCAACTTCAACAAGATCACCCCCAACCCCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAG 2496

Qy   132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCT 191
           ||| || || || ||| || ||| |||||||| || || || | | |||| |
Db   2497 CTGGCACACCAGTCCAACAGCACCAATATCTTCTTCCCCCCAGTGAGCATCGCTCAGACC 2556

Qy   192 TTCGGCCATGTTGAGTTTAGGTACTAAAGCCCATGAAGACAGAGATTTTAGAAGGTTTA 251
           || || || ||| ||| || | || |||| || || || || || ||| |
Db   2557 TTTGCAATGCTCTCCCCGGGACCAAGGCTGACACTCACGACTCGAAAATCCTGGAGGGCCTG 2616

Qy   252 AACTTTAATTTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTCAAGAGTTGTTG 311
           ||||| || ||| | |||| |||| | || ||| || || ||| ||||| | ||
Db   2617 AATTTCAACCTCACGGAGATTCCGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTC 2676

Qy   312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG 371
           ||| || || ||| ||| | || || || || || ||| |||| || |||| || |

Db   2677 CGTACCCTCAACCAGCAGACAGCAGCCAGCTCCAGCTGACCGACAGCCGCCAATGGCCGTGTTCCTC 2736

Qy   372 TCTGAAGGTTAAAATTGGTTGACAAATTCCTAGAGACGTCAAGAAACTATATCATAGT 431
           || || || ||||| ||| || |||| ||||| | || ||| |||| || | ||
Db   2737 AGCGAGGGCCTGAAGCTAGTGGTAAGTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 2796

Qy   432 GAGGCTTTACCGTTAATTTTGGTGATACTGAGCACCGAACACCAGCTAAAAGCAAATTAATGATTAT 491
           || ||| || ||| || ||||| || || ||| | || || | ||||| || || || ||||
Db   2797 GAAGCCTTCACTGTCAACTTCGGGGACCACCGAAGAGGCCAAGAAAACAGATCAACGATTAC 2856

Qy   492 GTTGAGAAAGGCACCCAGGGTAAGATCCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
           || || |||| || ||| || || |||| ||| |||||| || || | ||||| ||
Db   2857 GTGGAGAAGGGTACTCAAGGAGAAATAGTGTGGATTTGGTCAAGGAGGCTTGACAGAGACACA 2916

Qy   552 GTCTTCGCACTAGTTAACTATATTTTTCATGTTGATCAAGTACTACTGCTCTTTCGAGGTT 611
           ||||| | ||| ||||| ||||| || || || || || || | | |||
Db   2917 GTTTTTGCTCTGTCGATGAATTACATCTTCTTTAAAGGCAAATGGGAGACCCTTTGAAGTC 2976

Qy   612 AAAGATACTGAAGAGGAGAGATTTTCATGTTGATCAAGTACTACTGCTGCCACCGTGAAGTGCCTATG 671
           || | || ||| || || || || | || || || | | | || | || || || |||
Db   2977 AAGGACACCGAGGAAGAGGAGGAGGACTTCCAGTGGACCAGGTGACCACCCTGAAGTGCCTATG 3036

Qy   672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA 731
           ||||| | || || ||| | ||| || || || ||| || | || |||| |||
Db   3037 ATGAAGGCGTTTAGGCATGTTAACATCCAGCACTGTCGTAAGAGCTGTGTCCAGCTGGGTGCTG 3096

Qy   732 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTACCAGACGAAGGTAAGCTT 791
           ||||||| ||| | || | || || | || || || | || || || |
Db   3097 CTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAACTA 3156

Qy   792 CAACATTTAGAGAATAGAGTTGACTCATGACATTATTACTCATAATTTTTAGAACGAGGAT 851
           || ||| ||| ||||| || || | || ||||| | || | | ||| ||||
Db   3157 CAGCACCTGGAAAATGAACTCACCCCACGGATATCATCACCAAGTTCCTGGAAAATGAGAAC 3216

Qy   852 CGTCGTAGCGCTTCTCTGCCACCTGCCAAAGTTAAGATCATCACCGGTACTTACGACTTAAAA 911
           || ||| | || | | || | ||||| || || || |||| || | ||| ||| |
Db   3217 AGAAGGTGCCAGCTTACATTTACCCAAACTGTCCAAACTGTCGAACCTATGATCTGAAG 3276

Qy   912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTCTAACGTGCCGATTTGAGTGGT 971
           ||| ||||| || || || | ||||||||||| | |||||| || |||| ||
Db   3277 AGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGCTGACCTCTCCGGG 3336

Qy   972 GTTACTGAGAGAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT 1031
           || |||| || || || ||| || || | || || ||||||||| | || || ||
Db   3337 GTCACAGAGGAGGAGCACCCCTGAGCTCTCAAGGCCGCATAAGGCTGTGCTGACCATC 3396

Qy   1032 GATGAAAAGGGTACCGAGGCGCCGCCTATGTTCCTGGAAGCTATTCCAATGAGCATT 1091
           || ||||| | || || || || |||||| ||| || || || || | ||||
Db   3397 GACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATC 3456

Qy   1092 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGCAGAACACTAA 1151
           ||||||||||| || || || | || || || || ||||| || || ||
Db   3457 CCCCCGAGGTCAAGTTCAACAAACCCTTGTCTTCTTAATGATTGAACAAAATACCAAG 3516

Qy   1152 AGCCCATTGTTTATGGGTAAGGTTGTCAACCAACTCAGAA 1192
           || ||| ||| ||||||||||| || ||| | ||
Db   3517 TCTCCCCTCTTCATGGGAAAAGTGGTGAATCCACCCAAAA 3557

RESULT 11
US-09-299-141-10
; Sequence 10, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;   APPLICANT: FLOTTE, TERENCE R.
;   APPLICANT: SONG, SIHONG
;   APPLICANT: BYRNE, BARRY J.
;   APPLICANT: MORGAN, MICHAEL
;   TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;   FILE REFERENCE: 4300.011800
;   CURRENT APPLICATION NUMBER: US/09/299,141
;   CURRENT FILING DATE: 1999-04-23
;   EARLIER APPLICATION NUMBER: 60/083,025

```
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 10
;  LENGTH: 6924
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;  OTHER INFORMATION: p43msENCB-AT
US-09-299-141-10

Query Match             28.1%;    Score 429;  DB 4;  Length 6924;
Best Local Similarity   60.2%;    Pred. No. 1.1e-101;
Matches  711;  Conservative  0;  Mismatches  470;  Indels  0;  Gaps  0;

Qy    12 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAGACCAT 71
            ||||||| || ||| || |||| ||||| || |||| || |||| ||||||  ||| ||
Db  2377 GAGGATCCCCAGGGAGATGCGCCAGAAGACAGATACATCCCACCATGATCAGGATCAC 2436

Qy    72 AACTTTAATTTGACCGAAATCCAGAGCCCAAATTCACGAGGGTTTCAAGAGTTGTTG 131
            ||| || ||| |  || || || ||||  |||| || || |  |||   ||| ||
Db  2437 CCAACCTTCAACAAGATCACCCCCACCCCCAAATCTGCAGATTCCTGGGATCTCTATG 2496

Qy   132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTAGTCCTGTTCTATTGCCACTGCT 191
            || ||| ||| || || ||  |  || || ||||||| | || || |||  ||| ||
Db  2497 CTGGCACCACCAGTCCAACAGCCACCAATATCTTCTTCTCCCCAGTGCATCGCTACAGCC 2556

Qy   192 TTCGCCATGTTGAGTTTAGTTACTAAAGCCGATACCCATGACAGAGATTTTAGAAGGTTTA 251
            || || || ||  || || |||  ||| ||| | |||| ||| ||| || | |||| ||
Db  2557 TTTGCAATGCTCTCCCCTGGGACCAAGGCTCACACTCACGGTTTCAAGAGTTGTTG 2616

Qy   252 AACTTTAATTTGACCGAAATCCAGAGCCCAAATTCACGAGGGTTTCAAGAGTTGTTG 311
            ||| || ||| |  || || || ||||  ||| || ||| |  |||   ||| ||
Db  2617 AATTTCAACCTTCAACGATCCAGGGCTCAGATCCATGAAATCCTGGAGGCCTATACCGCCAG 2676

Qy   312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG 371
            || || || ||| ||| || || || || || || || || |||| |  || ||  || 
Db  2677 CGTACCCTCAACCAGCCAGACCAGCTCCAGCTGACCACTCCGACTGCCCTGTTCCTC 2736

Qy   372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 431
            || ||||  || ||| |||| || ||| || || ||| ||  ||  || ||||  | ||
Db  2737 AGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 2796

Qy   432 GAGGCTTTCACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT 491
            ||||| ||  || || || || || || |||| || ||| ||||  | || || ||
Db  2797 GAAGCCTTCACTGTCAACTTCGGGGACCACCTTCGGGGACCACCAGAGGCCAGAAACAGATCAACGATTAC 2856

Qy   492 GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
            || ||||  || || || || ||| ||  ||| |||| |||| |  ||| || ||| ||
Db  2857 GTGGAGAAGGGTACTCAGGGAACTCAGGGGAAATTGTGTCAAGGAGCTTGACAGAGACACA 2916

Qy   552 GTCTTCGCACTAGTAGTAACTATATTTTTTCAAGGTGAAGTTGGCAAGTGGGAACGTCCTTCCGAGGTT 611
            || || ||  | || || |||  ||||||||  ||| || || || || |||| ||| ||| ||||
Db  2917 GTTTTTGCTCTGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAACCCTTTGAAGTC 2976

Qy   612 AAAGATACTGAAGAGGAAGATTTTCATGTGATCAAGTTACTACTGTCAAAGTTCCAATG 671
            ||| | ||  ||| ||||| |||| ||| || ||  || || |  || ||||| ||||
Db  2977 AAGGACACCGAGGAAAGGAAGACTTCCCACGTCGACCAGTCCCCTGAGGTGCCTATG 3036

Qy   672 ATGAAAAGACTGGTATGTTCAATATTCAACATTGCAAAAATTAAGTTCTTGGGTCTTA 731
            || ||| || || |||| |||| || |||| || || || |  ||||| ||  || |
Db  3037 ATGAAGGCGTTTAGCCATGTTAACATCCAGAGTGTTAAGAGCTGTGTCCAGCTGGGTGCTG 3096

Qy   732 TTAATGAAGTATTAGGTAACCTACTGCTATTTTTTTACCACGAGAGGTAAGCTT 791
            || || || |  || ||  || || |  ||||||| ||| || || ||||
Db  3097 CTGATGAAATACCTGGCAATGCCAAGTTAGGTACTAAAGCCGATACCCATGAGGGGAAACTA 3156

Qy   792 CAACATTTAGAGAATGAAGTGAGTTGACACCTTGGGAAATGACTGTTTATTTAGAGAACGAGGAT 851
            ||||| || ||| || |||| |  ||  ||| || ||||| || |  ||||  || |  |||| 
Db  3157 CAGCACCTGGAAAATGAACTCACCCCACCCCCACGATATCATCCCACGATAAATGAGAAATGAAGAC 3216

Qy   852 CGTCGTAGCGCTTCTCTGCACCTGCCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA 911
            || || ||  || || || |  ||| ||||| || || |  | ||| |  || |  ||||
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Db  3217 AGAGGTCTGCCAGCTTACATTCAACTTACCCAAACTGTCCATTACTGGTGAACCTATGATCTGAAG 3276
            || || ||  ||| || |  || ||| || ||||  || |||| || ||| ||  ||||| ||||
Qy   912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAAGTTTTCTAACGGTGCCGATTTGAGTGGT 971
            || || |||| ||||| |  ||||| || ||| |||||||| ||| |||| |  |||
Db  3277 AGGGTCCTGGTCACTGGCATCACTAAGGTCTTCAGCAATGGGCCTGCACCTCTCCGGG 3336
            
Qy   972 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCAAAAACCGTCTTAACTATT 1031
            || || ||| || || |  ||||  || | ||| || |||| ||| ||| || |  |||
Db  3337 GTCACAGAGGAGGCACCCCCTGAAGCTCTCCAAGGCGTGCATAAGGGTGTGCTGACCATC 3396

Qy  1032 GATGAAAAGGTACCGAGGCCGCGGCCGCTGTATGTTCCTGGAAGCTATTCAATGAGACATT 1091
            || || ||||| ||| || ||| ||| |||  || || ||||  ||| ||||  || |||
Db  3397 GACCAGAAAGGGACTGAAGCTGCTGTGGGCCATGTTTTTAGAGGCCATACCCATGTCTATC 3456

Qy  1092 CCACCAGAAGTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGCAGGAACACTAAA 1151
            |  ||||||| ||||  || ||||  ||||| || || || |  || || ||| |  |
Db  3457 CCCCCGAGGTCAAGTTCAACAACCCTTTGTCTTCTTATGATTGAACAAAATACCCAG 3516

Qy  1152 AGCCCATTGTTATGGTAAGGTTGTCAACCCACTCAGAA 1192
            || |||||  | || || ||  | |  || ||| ||||
Db  3517 TCTCCCCTTCATGGGAAAAGTGGTGAATCCCACCCAAAA 3557


RESULT 12
US-09-299-141-11
;  Sequence 11, Application US/09299141
;  Patent No. 6461606
;  GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: 4300.011800
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: 60/083,025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 11
;  LENGTH: 6924
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;  OTHER INFORMATION: p43rmsENCB-AT
US-09-299-141-11

Query Match             28.1%;    Score 429;  DB 4;  Length 6924;
Best Local Similarity   60.2%;    Pred. No. 1.1e-101;
Matches  711;  Conservative  0;  Mismatches  470;  Indels  0;  Gaps  0;

Qy    12 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAGACCAT 71
            ||||||| || ||| || |||| ||||| || |||| || |||| ||||||  ||| ||
Db  2377 GAGGATCCCCAGGGAGATGCGCCAGAAGACAGATACATCCCACCATGATCAGGATCAC 2436

Qy    72 CCGACTTTTAATAAAATTACTCCAAATTAGCCGAATTTGCTTTCTTTGTTGTATAGACAA 131
            |  || |||| || || |||  ||| |||| ||| || ||||| ||  |  |  || ||
Db  2437 CCAACCTTTCAACAAGATCACCCCCACCCCCAAATCTGCAGATTCCTGGGATCTCTATG 2496

Qy   132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTAGTCCTGTTCTATTGCCACTGCT 191
            || ||| ||| || || ||  |  || || ||||||| | || || |||  ||| ||
Db  2497 CTGGCACCACCAGTCCAACAGCCACCAATATCTTCTTCTCCCCAGTGCATCGCTACAGCC 2556

Qy   192 TTCGCCATGTTGAGTTTAGTTACTAAAGCCGATACCCATGACAGAGATTTTAGAAGGTTTA 251
            || || || ||  || || |||  ||| ||| | |||| ||| ||| || | |||| ||
Db  2557 TTTGCAATGCTCTCCCCTGGGACCAAGGCTCACACTCACGGTTTCAAGAGTTGTTG 2616

Qy   252 CCGACTTTTAATAAAATTACTCCAAATTAGCCGAATTTGCTTTCTTTGTTGTATAGACAA 311
            |  || |||| || || |||  ||| |||| ||| || ||||| ||  |  |  || ||
Db  2617 CCAACCTTCAACAAGATCACCCCCACCCCCAAATCTGCAGATTCCTGGGATCTCTATG 2676

Qy   312 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTAGTCCTGTTCTATTGCCACTGCT 371
            || ||| ||| || || ||  |  || || ||||||| | || || |||  ||| ||
Db  2677 CTGGCACCACCAGTCCAACAGCCACCAATATCTTCTTCTCCCCAGTGCATCGCTACAGCC 2736

Qy   432 GAGGCTTTCACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT 491
            ||||| ||  || || || || || || |||| || ||| ||||  | || || ||
Db  2797 GAAGCCTTCACTGTCAACTTCGGGGACCACCAGAGGCCAGAAACAGATCAACGATTAC 2856

Qy   492 GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC 551
            || ||||  || || || || ||| ||  ||| |||| |||| |  ||| || ||| ||
Db  2857 GTGGAGAAGGGTACTCAGGGAACTCAGGGGAAATTGTGTCAAGGAGCTTGACAGAGACACA 2916

Qy   552 GTCTTCGCACTAGTAGTAACTATATTTTTTCAAGGTGAAGTTGGCAAGTGGGAACGTCCTTCCGAGGTT 611
            || || ||  | || || |||  ||||||||  ||| || || || || |||| ||| ||| ||||
Db  2917 GTTTTTGCTCTGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAACCCTTTGAAGTC 2976

Qy   612 CCGACTTTTAATAAAATTACTCCAAATTAGCCGAATTTGCTTTCTTTGTTGTATAGACAA 671
            |  || |||| || || |||  ||| |||| ||| || ||||| ||  |  |  || ||
Db  2977 CCGACTTTTAATAAAATTACTCCAAATTAGCCGAATTTGCTTTCTTTGTTGTATAGACAA 3036

Qy   132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTAGTCCTGTTCTATTGCCACTGCT 191
            || ||| ||| || || ||  |  || || ||||||| | || || |||  ||| ||
Db  2497 CTGGCACCACCAGTCCAACAGCCACCAATATCTTCTTCTCCCCAGTGCATCGCTACAGCC 2556

Qy   192 TTCGCCATGTTGAGTTTAGTTACTAAAGCCGATACCCATGACAGAGATTTTAGAAGGTTTA 251
            || || || ||  || || |||  ||| ||| | |||| ||| ||| || | |||| ||
Db  2557 TTTGCAATGCTCTCCCCTGGGACCAAGGCTCACACTCACGGTTTCAAGAGTTGTTG 2616

Qy    72 CCGACTTTTAATAAAATTACTCCAAATTAGCCGAATTTGCTTTCTTTGTTGTATAGACAA 131
            |  || |||| || || |||  ||| |||| ||| || ||||| ||  |  |  || ||
Db  2437 AATTTCAACCTTCAACGATCCAGGGCTCAGATCCATGAAATCCTGGAGGCCTATACCGCCAG 2496

Qy   252 AACTTTAATTTGACCGAAATCCAGAGCCCAAATTCACGAGGGTTTCAAGAGTTGTTG 311
            ||| || ||| |  || || || ||||  ||| || ||| |  |||   ||| ||
Db  2617 AATTTCAACCTTCAACGATCCAGGGCTCAGATCCATGAAATCCTGGAGGCCTATACCGCCAG 2676
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; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
; LENGTH: 6981
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID C-AT2
US-09-299-141-7

Query Match         28.1%;    Score 429;  DB 4;  Length 6981;
Best Local Similarity  60.2%;    Pred. No. 1.1e-101;
Matches  711;  Conservative  0;  Mismatches  470;  Indels  0;  Gaps  0;

Qy     12 GAAGACCCTCAAGGCGACGCCGCTCAAAAAACCGACACCAGTCATCACGACCAAGACCAT   71
          || |||| ||   |||| |  || | |||||||  | | | ||  || ||| | |||| |
Db    165 GAGGATCCCCAGGGAGGATGCTGCCCAGAAGACAGATACATCCCACCCATGATCAGGATCAC  224

Qy     72 CCGACTTTAATAAAATTACTCCAAATTTAGCCGAATTTGCTTTTTCTTTGTATAGACAA  131
          ||  | ||| |  ||||| |||| |  | | | | || ||| | || || ||||
Db    225 CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAG  284

Qy    132 TTAGCTCATCAAAGTAATTCTACTAACATTTTTTAGTCTGTTCTTATTGCCACTGCT  191
          || || |||| |  |||| | | || || | || |  | |  | |  ||| | |
Db    285 CTGGCACCACCAGTCCAACAGCAACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCC  344

Qy    192 TTCGCCATGTGAGTTAGGTACTAAAGCCGATACCAAGGTTAGAAGGTTTA  251
          ||  | ||  | || | | | |   || || | | ||  | | |  || |
Db    345 TTTGCAATGCTCTCCCCTGGGGACCAAGGCTGACACTGACAGCTGAAAATCCTGGAGGGCCTG  404

Qy    252 AACTTTAATTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTCAAGAGTTGTTG  311
          |||| | |||| | | | |    |   | | ||  | || || | |||  || || ||
Db    405 AATTTCAACCTCACGGAGATTCCGGAGCTCAGATCCATGAAGGCCTCCAGGAACTCCTC  464

Qy    312 AGAACTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTTTATTTTG  371
          | |||||||| |   ||| |||| | ||||| | | ||| || ||| |||||
Db    465 CGTACCCTCAACCAGCCAGACAGCAGCTCCAGCTGACCACCGGCCAATGCCCTGTTCCTC  524

Qy    372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAGACGTCAAGAACTATATCATAGT  431
          | |||| | || ||||| ||||| |||| |  |||||  | |||||  | | ||| | |
Db    525 AGCGAGGGGCCTGAAGCTAGTGGATAAGTTTTGGAGGATGTTAAAAAGTGTACCACTCA  584

Qy    432 GAGGCTTTTACCCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT  491
          |||| ||| | ||| | |||| |||| | | | || || ||||||| | ||| |  ||||
Db    585 GAAGCCTTCACTGTCAACTTCGGGGACCGAGGAGGCCGAAGAGAACAGATCAACGATTAC  644

Qy    492 GTTGAGAAAGGCACCCAGGTAAGATCGTTGACCTAGTTAAAGAATTAGGATCGTGATACC  551
          |||||||||| || |||| || | | |||| | || | ||| ||| | | |  ||| ||
Db    645 GTTGAGAAAGGCACCCACCGGGCTAAGAATTCGTGTTCACAAATCGTGTTGGATTGGTGATACC  704

Qy    552 GTCTTCGCACTAGTTAACTATAT  611
          || || |||| ||| || | |||
Db    705 GTTTTTGCTCTGGTGTAACCTTGAATTACATCTTCTTTAAAGGCAAGCAAATGGGACACCCCTTTGAAGTC  764

Qy    612 AAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG  671
          | ||| ||| |||||||||||| | |||  || | |||| || |||| | |||| |||
Db    765 AAGGACACCGAGGAGAGGGACTTCCACGTGACCACCGTGAAGGTGCCTATG  824

Qy    672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAAATTAAGTTCTTGGGTCTTA  731
          || |||| |||||| || || ||  | ||| ||||| | | | | ||| | |||||
Db    825 ATGAGAGCGTTTAGGCATGTTAACATCCAGCACTGTAAGAAGCTGTCCAGCTGGCTGGTGCTG  884

Qy    732 TTAATGAAGTATTAGGTAACGCTACTGCTATTTTTTTTTTTTTACCAGACAGCGAAGGTAAGCTT  791
          | ||||| | || | || || |  || | ||| | ||
Db    885 CTGATGAAATACCTGGGCAATGCCAGCCATCTTCTTCTTCGCCTGCCTCGTGTCGGTCGGGAAACTA  944

Qy    792 CAACATTTAGAGAATGAGTTGACTCATGACAATATTATTCAACAGGAGGAT  851
          ||||  ||| |  || |||  | | |  |  | |||| | ||||| |||||
Db    945 CAGCCACCTGGAAATGAACTCACCCACGATATCATCACCAGTTCCTGGAAATGAAGAC  1004
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Qy    312 AGAACTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTTTATTTTTG  371
          | |||||||| |  | ||| |||| | ||||| | | ||| || ||| |||||
Db   2677 CGTACCCTCAACCAGCCAGACAGCAGCTCCAGCTGACCACCGGCCAATGCCCTGTTCCTC  2736

Qy    372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAGACGTCAAGAACTATATCATAGT  431
          | |||| | || ||||| ||||| |||| |  |||||  | |||||  | | ||| | |
Db   2737 AGCGAGGGGCCTGAAGCTAGTGGATAAGTTTTGGAGGATGTTAAAAAGTGTACCACTCA  2796

Qy    432 GAGGCTTTTACCCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT  491
          |||| ||| | ||| | |||| |||| | | | || || ||||||| | ||| |  ||||
Db   2797 GAAGCCTTCACTGTCAACTTCGGGGACCGAGGAGGCCGAAGAGAACAGATCAACGATTAC  2856

Qy    492 GTTGAGAAAGGCACCCAGGTAAGATCGTTGACCTAGTTAAAGAATTAGGATCGTGATACC  551
          |||||||||| || |||| || | | |||| | || | ||| ||| | | |  ||| ||
Db   2857 GTGGAGAAGGGTACTCAAGGGAAAAATGTTGGATTTGGTGATGAGGAGCTTGACAGAGACACA  2916

Qy    552 GTCTTCGCACTAGTTAACTATAT  611
          || || |||| ||| || | |||
Db   2917 GTTTTGCTCTGGTGAATTACATCTTCTTTAAAGGCAAATGGCAAATGGGAACCCTTTGAAGTC  2976

Qy    612 AAAGATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG  671
          | ||| ||| |||||||||||| | |||  || | |||| || |||| | |||| |||
Db   2977 AAGGACACCGAGGAAGAGACTTCCACGTGACCACCGTGAGGTGCCTATG  3036

Qy    672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAAATTAAGTTCTTGGGTCTTA  731
          || |||| |||||| || || ||  | ||| ||||| | | | | ||| | |||||
Db   3037 ATGAGGCGTTTAGGCATGTTAACATCCAGCACTGTAAGAGCTGTCCAGCTGGCTGTGCTG  3096

Qy    732 TTAATGAAGTATTAGGTAACGCTACTGCTATTTTTTTTTTTTTTACCAGACAGCGAAGGTAAGCTT  791
          | ||||| | || | || || |  || | ||| | ||
Db   3097 CTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCTGCCTGCCTCGTGTCGGTCGGGAAACTA  3156

Qy    792 CAACATTTAGAGAATGAGTTGACTCATGACAATATTATTCAACAGGAGGAT  851
          ||||  ||| |  || |||  | | |  |  | |||| | ||||| |||||
Db   3157 CAGCCACCTGGAAATGAACTCACCCACGATATCATCACCAGTTCCTGGAAATGAAGAC  3216

Qy    852 CGTCGTAGCCGTTCTCTGCACCTGCCAAAGTAAGTAATCACCGGTACTTACGACTTAAAA  911
          || ||| |||||| | ||| || | ||||| ||| |  |||| ||| |  |||| ||||
Db   3217 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAG  3276

Qy    912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAAGTTTTTCTAACGGTGCCGATTTGAGTGGT  971
          | |||| |||| ||| | |||| |  ||||   ||| || | |||| |
Db   3277 AGCGTCTGGGTCAACTGGCATCATCAGGGCTCTTCAGCAATGGGCTGACCTCTCCGGG  3336

Qy    972 GTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCCGTCTTCACAAAGCCGTCTTAACTATT  1031
          || | |||| |||| | || | |||||| ||||| | | || |
Db   3337 GTCACAGAGGAGGCACCCCGTGAAGCTCCCAGGCCGTCTCGATAAGGCTGTCTGCGACCATC  3396

Qy   1032 GATGAAAAGGTACCGAGGCCGCCGGCCGCGCTATGTTCCTGGAAGCTATTCCAATGAGCATT  1091
          |||||| |||||| ||||| | | |||| |  || |||| | | || ||| || ||||| ||
Db   3397 GACGAGAAAGGGACTGAGCTGCTGGGCCATGAACCCATGTCTATC  3456

Qy   1092 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGCAGAACACTAAA  1151
          | |||| |||||| | |||| | | || |||||| | ||| || |  ||||| ||||||
Db   3457 CCCCCGAGGTCAAGTTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAG  3516

Qy   1152 AGCCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAA  1192
          | |||||| ||| |  || | | |||| ||||| |||||||
Db   3517 TCTCCCCTCTTCATGGGAAAAGTGTGAATCCACCCAAAA  3557
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RESULT 13
US-09-299-141-7
; Sequence 7, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
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Qy   852  CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA   911
              |||||| ||  |||||||||||  |||  ||| || ||  |  ||
Db  1005  AGAAGGTCTGCCAGCTTACATTTACCAAAACTGTCCATTACTGGAACCTATGATCTGAAG  1064

Qy   912  TCTGTTTAGGCCAGTAGTATTACCAAAGTTTTTCTAACGTGCCGATTTGAGTGGT        971
              || |||| |||||||||  ||  ||||  ||||| ||  ||  || |||
Db  1065  AGCGTCCTGGGTCAACTGGCATCACTAAGGTCTTCAGCAATGGGCGCTGACCTCTCCGGG  1124

Qy   972  GTTACTGAAGAGAGTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT  1031
              || ||| || |||||  ||  ||||  |||||| || || |||
Db  1125  GTCCACGAGAGAGGCACCCCTGAAGCTCTCCAAGGCGTGCATAAGGCGTGCTGCTGACCATC  1184

Qy  1032  GATGAAAAGGTACCGAGGCCGCGGCGTATGTTCCTGAAGCTATTCCAATGAGCATT      1091
              || |||| |||  ||  |||| ||||  ||||||   |  |||  ||
Db  1185  GACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGGGCCATACCCATGTCTATC  1244

Qy  1092  CCACCAGAAGTTAAATTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA   1151
              |||| || |||| || |  |||  ||| |||||||| |  || ||||
Db  1245  CCCCCGAGGTCAAGTCAACAAAACCCTTTGTCTTCCTTAATGATTGAACAAAATACCAAG  1304

Qy  1152  AGCCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAA  1192
              ||   |  ||| ||||| |||  ||  ||  ||  ||
Db  1305  TCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAA  1345
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RESULT 14
US-09-299-141-3
; Sequence 3, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;   APPLICANT: FLOTTE, TERENCE R.
;   APPLICANT: SONG, SIHONG
;   APPLICANT: BYRNE, BARRY J.
;   APPLICANT: MORGAN, MICHAEL
;   TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;   FILE REFERENCE: 4300.011800
;   CURRENT APPLICATION NUMBER: US/09/299,141
;   CURRENT FILING DATE: 1999-04-23
;   EARLIER APPLICATION NUMBER: 60/083,025
;   EARLIER FILING DATE: 1998-04-24
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 7054
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID dE-AT
US-09-299-141-3

Query Match   28.1%; Score 429; DB 4; Length 7054;
Best Local Similarity 60.2%; Pred. No. 1.1e-101;
Matches 711; Conservative   0; Mismatches 470; Indels   0; Gaps   0;

```
Qy    12  GAAGACCCTCAAGGCGACGACGCGCTCAAAAAACCGACCACCAGTCATCACGACCAGACCAT   71
              || |||| |||||| || ||  ||   ||||  |||  || ||  ||
Db  1433  GAGGATCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCACCATGATCAGGATCAC  1492

Qy    72  CCGACTTTAATAAAATTACTCCAAATTAGCCGAATTGCTTTTTCTTTGTTATAGACAA    131
              || |  ||  |  ||  |||  ||  ||| |||  || ||| |  ||
Db  1493  CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCCAG  1552

Qy   132  TTAGCTCATCAAAGTAATTCTACTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCT    191
              |||| |||  |  ||   ||  |  ||||||||| ||||||  |||  |  || |||
Db  1553  CTGGCACCACCAGTCCAACAGCACCAATATCTTCTCTTCCCCAGTGAGCATCGCTACAGCC  1612

Qy   192  TTCGGCCATGTGAGTTTGAGTTTAGGTACTAAAGCCCATGACCATGCGAGATTTTAGAAGGTTTA   251
              || |||||||  ||||| || |||||| ||  || |||  ||| ||
Db  1613  TTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTG  1672

Qy   252  AACTTTAATTCACCGAAATCCCAGAGAGCCCAAATTCACGAGGTTTTCAAGAGTTGTTG    311
              || |  ||  | || ||  ||  |||  || |||  |||  ||  || || |||
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```
Db  1673  AATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAGAAGGCTTCCAGGAACTCCTC  1732

Qy   312  AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTG   371
              || |  || |||| || ||| ||  ||| ||  || |  ||  |  ||
Db  1733  CGTACCCTCAACCAGCCAGCAGCCGAGCTCCAGCTGACCACCACCGGCCTGTTCCTC  1792

Qy   372  TCTGAAGTTTAAAATTGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT   431
              || |||| || || |  || |||  || ||  || ||  ||  ||  ||||  |||
Db  1793  AGCGAGGGCCTGAAGCTAGTGGATAAGTTTTGGAGGATGTTAAAAGTGTACCACTCA  1852

Qy   432  GAGGCTTTTACCGTTAATTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT   491
              || || ||| || ||  || || || || || |||| || |||  ||||  ||||  ||
Db  1853  GAAGCCTTCACTGTCAACTTCGGGGACACCGAGAGGCCAAGAAACAGATCAACGATTAC  1912

Qy   492  GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC   551
              || ||||| || ||  |||  ||| |  |||  || ||||||| ||  ||  || |||||
Db  1913  GTGGAGAAGGGTACTCAAGGGAAAATTGTGATTTGGTCAAGGAGCTTGACAGAGACACA  1972

Qy   552  GTCTTCGCACTAGTTAACTATATTTTTCAAGGTAAGTGGGAACGTCCTTTCGAGGTT    611
              || ||| | || || ||  ||  ||  ||||  || ||| | |  ||||  || |||
Db  1973  GTTTTTGCTCTGGTGAATTACATCTTCTTTAAAGGCAATGGGAAGCAAGTCTTGAAGTC  2032

Qy   612  AAAGATACTGAAGAGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAGTTCCAATG    671
              || ||  | |||| ||  | |||||||| |||||| || ||||  ||  |||  ||
Db  2033  AAGGACACCGAGGAAGAGGACTTCCACGTGACCAGGTGACCACCGTGAAGGTGCCTATG  2092

Qy   672  ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA   731
              |||||  | ||| ||||||| || ||| || || | || ||  ||  || ||||| ||
Db  2093  ATGAAGCGTTTAGGCATGTTAACATCCAGCACTGTAAGAAGCTGTCCAGCTGGTGCTG  2152

Qy   732  TTAATGAAGTATTAGGTAACGCTACTGCTATTTTTTTTTTTTACCAGGACGAAGTAAGCTT   791
              |  ||||| ||||| |||| | |||  ||| ||  ||  ||  |||||  || || |||
Db  2153  CTGATGAAATACCTGGCAATGCCCATCTTCTTCCTGCCTGATGAGGGGAAACTA  2212

Qy   792  CAACATTTAGAAGATGAGTAGTGACTCATGACATTATAAATTTTAGAGAACGAGGAT   851
              ||  | ||| |  |  || || ||  |||| ||| || || ||  ||||| ||| ||
Db  2213  CAGCACCTGAAAATGAACTCACCCACGATATCATCACCCAAGTTCCTGAAAATGAAGAC  2272

Qy   852  CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAA   911
              |||||| ||  |||||||||||  |||  ||| || ||  |  ||
Db  2273  AGAAGGTCTGCCAGCTTACATTTACCAAAACTGTCCATTACTGGAACCTATGATCTGAAG  2332

Qy   912  TCTGTTTAGGCCAGTAGTATTACCAAAGTTTTTCTAACGTGCCGATTTGAGTGGT        971
              || |||| |||||||||  ||  ||||  ||||| ||  ||  || |||
Db  2333  AGCGTCCTGGGTCAACTGGCATCACTAAGGTCTTCAGCAATGGGCGCTGACCTCTCCGGG  2392

Qy   972  GTTACTGAAGAGAGTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATT  1031
              || ||| || |||||  ||  ||||  |||||| || || |||
Db  2393  GTCACAGAGAGGAGGCACCCCTGAAGCTCTCCAAGGCGTCCCATAAGCCGTGCTGCCATC  2452

Qy  1032  GATGAAAAGGTACCGAGGCCGCGGCGTATGTTCCTGAAGCTATTCCAATGAGCATT      1091
              || |||| |||  ||  |||| ||||  ||||||   |  |||  ||
Db  2453  GACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGGGCCATACCCATGTCTATC  2512

Qy  1092  CCACCAGAAGTTAAATTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA   1151
              |||| || |||| || |  |||  ||| |||||||| |  || ||||
Db  2513  CCCCCGAGGTCAAGTCAACAAAACCCTTTGTCTTCCTTAATGATTGAACAAAATACCAAG  2572

Qy  1152  AGCCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAA  1192
              ||   |  ||| ||||| |||  ||  ||  ||  ||
Db  2573  TCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAA  2613
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RESULT 15
US-09-299-141-2
; Sequence 2, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;   APPLICANT: FLOTTE, TERENCE R.
;   APPLICANT: SONG, SIHONG
;   APPLICANT: BYRNE, BARRY J.
;   APPLICANT: MORGAN, MICHAEL
;   TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY

```
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID E-AT
US-09-299-141-2

Query Match       28.1%;    Score 429; DB 4;  Length 7405;
Best Local Similarity   60.2%;   Pred. No. 1.1e-101;
Matches   711;  Conservative   0; Mismatches 470;  Indels   0;  Gaps   0;

Qy    12 GAAGACCCTCAAGGCGCACCGCCGCTCAAAAAACCGACACCAGTCATCACGACCAAGACCAT    71
         ||| || | || |  |||| || | |||   |    ||  || |||| ||   |  ||
Db  1784 GAGGATCCCCAGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCAC   1843

Qy    72 CCGACTTTTAATAAAATTACTCCAAATTAGCCGAATTGCTTTTCTTTGTTATAGACAA    131
         || | | ||   | | || | ||   ||| |||| || | |||| |    || | ||
Db  1844 CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCGCCTATACCGCCAG   1903

Qy   132 TTAGCTCATCAAAGTAATTCTACTAACATATTTTTTAGTCCTGGTTTCTATTGCCACTGCT    191
         || || ||||  | |||  | || |||  ||   ||| |   |  || | | |||| |||
Db  1904 CTGGCACACCAGTCCAACAGCCACCAATATCTTCTTCTCCCCAGTGACGATCGCTACAGCC   1963

Qy   192 TTCGCCATGTGAGTTTAGGTACTAAAGCCGATACCCAGTGAAGAGATTTAGAAGGTTTA    251
         || ||  ||| | || | || |||||| | |||| || ||| | || |||| ||| ||
Db  1964 TTTGCAATGCTCTCCCTGGGACCAAGGCTCGACACTCAGGCGATGAAATCCTGGAGGGCCTG   2023

Qy   252 AACTTTAATTCCCAGAAGCCCAAATTCACGGAGGTTTCAAGAGTTGTTG    311
         |||  |||  |||||||| ||||  | |||||| | ||| || || |
Db  2024 AATTTCAACCTCACGGAGATTCCGGAGGCCTCAGATCCCATGAAGCCTTCCAGGAACTCCTC   2083

Qy   312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGTGAACGGTTTATTTTTG    371
         || |  |||||  |||| || ||  ||  |||| |||  || || |    || |  |||
Db  2084 CGTACCCTGCAACAGCCCAGACAGCCTGACTCCAGCTGACCACCGCAATGCCGTGTTCCTC   2143

Qy   372 TCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT    431
         | ||| || ||||| | |||||||| |  |||| ||| || ||||| ||||| || |
Db  2144 AGCGAGGGCCTGAAGCTAGTGACAACTTCGGGGGACACCGGATAAGTTTTTGGAGGATGT   2203

Qy   432 GAGGCTTTTACCGTTAATTTGGTGATACTGAGGAAGTAAAAGCAAATTAATGATTAT    491
         |||||  | || || |||| ||| |  | ||  || ||||| |||  ||| ||||
Db  2204 GAAGCCTTCACTGTCAACTTCGGGGACACCGGACCAAGAGGCCAAGAAACAGATCAACGATTAC   2263

Qy   492 GTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACC    551
         || |||||| | || |||||| |||   ||| | ||| ||| |||| || | |||| |
Db  2264 GTGGAGAAGGGTACTCAGGGTCAAGGGAAAAATTGTGGATTTGGTCAAGGGCTAGTAGC   2323

Qy   552 GTCTTCGCACTAGTTAACTAATATTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTT    611
         || ||| | ||| | |||  |||| ||  |||| || || |||| | ||||| |||| |
Db  2324 GTTTTTGCTCTGGTGAATTACATCTTTCTTAAAGGCAAATGGGAGAGACCCTTTGAAGTC   2383

Qy   612 AAAGATACTGAAGGAAGAAGATTTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAATG    671
         ||||| ||||| ||||| |||  || | || || ||| | ||  ||  ||||| || ||
Db  2384 AAGGACACCGAGGAAGAGGAGACTTCCACGTGGACCAGTGACCACCGTGAAGGTGCCTATG   2443

Qy   672 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA    731
         |||||  | | ||| |||||| |||| | |||| | ||||| ||| | || ||||| ||
Db  2444 ATGAAGCGGTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAGCTGGGTGCTTG   2503

Qy   732 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTTTACCAGACGAAGTAAGCTT    791
         | ||||||  | || |   ||| | ||| |  | ||| || ||| | ||| | | ||
Db  2504 CTGATGAAATACCTGGCAATGCCATCCTTCTTCCTGCCTGATGCTGAGGGGAAACTA   2563

Qy   792 CAACATTTAGAGAATGAGTTGACTCATGACATTATTACTACTAAATTTTAGAGAACGAGGAT    851
         | ||| || || |  || ||||| || |||||| ||| ||| |||| | |||| |||||

Db  2564 CAGCACCTGGAAAATGAACTCACCCACGATATCATCACCAAGAGTTCCTGAAAATGAGAC   2623
Qy   852 CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTACGTTAAGTATCACCGGTACTTACGACTTAAAA    911
         || || ||||  | || || || || |||||| ||| | |||||| |||| |||| ||||
Db  2624 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTTACTGGAACCTATGATCTGAAG   2683
Qy   912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAGTTTTTCTAACGGTGCCGATTTGAGTGGT    971
         ||| | || || |||| |||  | || ||||| |  |  | || || ||| |||| ||
Db  2684 AGCGTCCTGGGTCAACTGGCATCACTAAGGTCTTCAGCAATGGGCGTGACCTCTCCGGG   2743
Qy   972 GTTACTGAAGAAGCTCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTCAACTATT   1031
         || ||  ||||||   ||  |||  || || || ||||||   |||| |  || ||| ||
Db  2744 GTCACAGAGGAGGAGGCACCCCTGAAGCTCTCCAGGCCGTGCATAAGGCTGTGTGCGACCATC   2803
Qy  1032 GATGAAAAGGGTACCAGGCGCCGGCCGATGTCCTGGAAGCTATTCCAATGAGCATT   1091
         |||||||| ||| | |  || || || ||| ||||| ||| ||||||||| |||
Db  2804 GACGAGAAAGGGACTGAAGCTGCTGGGGCCCATGTTTTTAGAGGCCATACCCATGTCTATC   2863
Qy  1092 CCACCAGAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGCAGAACACTAAA   1151
         | |||||| | ||||| || |||| || | ||| | ||||| | || |||||||| | |
Db  2864 CCCCCCGAGGTCAAGTTCAACAAACCTTTGTCTTCTTAATGATTGAACAAAATACCAAG   2923
Qy  1152 AGCCCATTGTTTATGGGTAAGGTTGTCAACCCAACTCAGAA   1192
         |  || |  ||||| ||| ||| ||  ||||| |||||||
Db  2924 TCTCCCCTTCTTCATGGGAAAAGTGTGAATCCCACCCCAAAA   2964

Search completed: December   6, 2002, 23:35:50
Job time : 88 secs
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